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*** YOU HAVE NEW MAIL ***

=> s nucleic acid
   4 FILES SEARCHED...
L1      343861 NUCLEIC ACID

=> s l1 and positiv? (3a) charge tag (3a) nucleic acid?
L2           2 L1 AND POSITIV? (3A) CHARGE TAG (3A) NUCLEIC ACID?

=> d l2 bib abs 1-2

L2   ANSWER 1 OF 2  WPIDS (C) 2002 THOMSON DERWENT
AN   2002-674850 [72]   WPIDS
CR   1997-393613 [36]
DNC  C2002-190055
TI   Composition useful for e.g. separation of nucleic acids comprises a
     positively or neutrally charged phosphoramidite.
DC   B04 B05 D16
IN   ALLAWI, H T; LYAMICHEV, V; NERI, B P; SKRZPCZYNSKI, Z; TAKOVA, T; WAYLAND,
     S R
PA   (THIR-N) THIRD WAVE TECHNOLOGIES INC
CYC  100
PI   WO 2002063030 A2 20020815 (200272)* EN  197p
        RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ
            NL OA PT SD SE SL SZ TR TZ UG ZM ZW
         W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK
            DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR
            KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT
            RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM
            ZW
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US 2002128465 A1 20020912 (200272)
ADT WO 2002063030 A2 WO 2002-US3423 20020206; US 2002128465 A1 CIP of US 1996-682853 19960712, CIP of US 1999-333145 19990614, US 2001-777430 20010206
FDT US 2002128465 A1 CIP of US 6001567
PRAI US 2001-777430 20010206; US 1996-682853 19960712; US 1999-333145 19990614
AN 2002-674850 [72] WPIDS
CR 1997-393613 [36]
AB WO 200263030 A UPAB: 20021108

NOVELTY - Composition comprises a positively or neutrally charged phosphoramidite.

DETAILED DESCRIPTION - Composition (c) or (c') comprises a positively charged phosphoramidite of formula (I) or a neutrally charged phosphoramidite of formula (II). (I) comprises nitrogen-containing chemical group selected from primary, secondary or tertiary amine or ammonium group. (II) comprises secondary or tertiary amine or ammonium group.

X, Z = a reactive phosphate group;
Y = a protected hydroxy group;
X' = a protected hydroxy group;
N, N' = an amine group.

INDEPENDENT CLAIMS are included for the following:

(1) a composition (c1) comprising a charge tag (x1) attached to a terminal end of a **nucleic acid** molecule, the charge tag comprises a phosphate group and a positively charged molecule;

(2) a composition (c2) comprising a **nucleic acid** molecule that comprises a positively charged phosphoramidite;

(3) a composition (c3) comprising a charge tag attached to the terminal end of a **nucleic acid** molecule, the **charge tag** comprises a **positively** charged phosphoramidite;

(4) a composition (c4) comprising a fluorescent dye directly bonded to a phosphate group, which is not directly bonded to an amine group;

(5) a mixture (m) comprising a number of oligonucleotides, each oligonucleotide is attached to a different charge tag with each charge tag comprising a phosphate group and a positively charged group;

(6) a composition (c5) comprising a solid support attached to a charged tag, the charge tag comprises a positively charged group and a reactive group configured to allow the charge tag to covalently attach to the **nucleic acid** molecule;

(7) separating **nucleic acid** molecules involving either:

(a) treating (m1) a charge-balanced oligonucleotide containing the charge tag to produce a charge-unbalanced oligonucleotide and separating the charge-unbalanced oligonucleotide from the reaction mixture; or

(b) treating (m2) a number of charge-balanced oligonucleotides, each containing different charge tags, to produce at least 2 charge-unbalanced oligonucleotides, and separating the charge-unbalanced oligonucleotides from the reaction mixture.

USE - The composition is useful for separation of **nucleic acid** molecules (claimed). The composition is further useful for fractionation of specific nucleic acids by selective charge reversal useful in e.g. INVADER assay cleavage reactions; and in the synthesis of charge-balanced molecules.

ADVANTAGE - In the fractionation of **nucleic acid** molecules, the method provides an absolute readout of the partition of products from substrates (i.e. provides a 100% separation). Through the use of multiple positively charged adducts, synthetic molecules can be constructed with sufficient modification due to the fact that the normally negatively charged strand is made nearly neutral. It is also possible to distinguish between a enzymatically or thermally degraded DNA fragments

due to the absence or presence of 3'phosphate.
Dwg.0/46

L2 ANSWER 2 OF 2 USPATFULL
AN 2002:236261 USPATFULL
TI Charge tags and the separation of **nucleic acid** molecules
IN Lyamichev, Victor, Madison, WI, UNITED STATES
Skrzpczynski, Zbigniew, Verona, WI, UNITED STATES
Allawi, Hatim T., Madison, WI, UNITED STATES
Wayland, Sarah R., Madison, WI, UNITED STATES
Takova, Tsetska, Madison, WI, UNITED STATES
Neri, Bruce P., Madison, WI, UNITED STATES
PA Third Wave Technologies, Inc. (U.S. corporation)
PI US 2002128465 A1 20020912
AI US 2001-777430 A1 20010206 (9)
RLI Continuation-in-part of Ser. No. US 1999-333145, filed on 14 Jun 1999, PENDING Continuation-in-part of Ser. No. US 1996-682853, filed on 12 Jul 1996, GRANTED, Pat. No. US 6001567
DT Utility
FS APPLICATION
LREP MEDLEN & CARROLL, LLP, 101 HOWARD STREET, SUITE 350, SAN FRANCISCO, CA, 94105
CLMN Number of Claims: 86
ECL Exemplary Claim: 1
DRWN 46 Drawing Page(s)
LN.CNT 5163
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to novel phosphoramidites, including positive and neutrally charged compounds. The present invention also provides charge tags for attachment to materials including solid supports and nucleic acids, wherein the charge tags increase or decrease the net charge of the material. The present invention further provides methods for separating and characterizing molecules based on the charge differentials between modified and unmodified materials.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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=> d his

     (FILE 'HOME' ENTERED AT 10:12:59 ON 18 DEC 2002)

     FILE 'BIOSIS, MEDLINE, CAPLUS, WPIDS, USPATFULL' ENTERED AT 10:13:34 ON
     18 DEC 2002
L1       343861 S NUCLEIC ACID
L2            2 S L1 AND POSITIV? (3A) CHARGE TAG (3A) NUCLEIC ACID?

=> s l1 and positiv? (4a) charg? (3a) tag?
L3           21 L1 AND POSITIV? (4A) CHARG? (3A) TAG?

=> s l3 not l2
L4           19 L3 NOT L2

=> dup rem l5
L5 IS NOT VALID HERE
The L-number entered has not been defined in this session, or it
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=> dup rem l4
PROCESSING COMPLETED FOR L4
L5            19 DUP REM L4 (0 DUPLICATES REMOVED)

=> d l5 bib abs 1-19

L5   ANSWER 1 OF 19  USPATFULL
AN     2002:329813  USPATFULL
TI     Mutation analysis by mass spectrometry using photolytically cleavable
       primers
IN     Kostrzewa, Markus, Borsdorf-Panitzsch, GERMANY, FEDERAL REPUBLIC OF
       Frohlich, Thomas, Leipzig, GERMANY, FEDERAL REPUBLIC OF
       Wenzel, Thomas, Leipzig, GERMANY, FEDERAL REPUBLIC OF
       Jaschke, Andres, Berlin, GERMANY, FEDERAL REPUBLIC OF
       Hausch, Felix, Stanford, CA, UNITED STATES
PA     Bruker Saxonia Analytik GmbH, Leipzig, GERMANY, FEDERAL REPUBLIC OF
       (non-U.S. corporation)
PI     US 2002187493      A1   20021212
AI     US 2002-79043      A1   20020220 (10)
PRAI   DE 2001-108453      20010222
DT     Utility
FS     APPLICATION
LREP   KUDIRKA & JOBSE, LLP, ONE STATE STREET, SUITE 1510, BOSTON, MA, 02109
CLMN   Number of Claims: 22
ECL    Exemplary Claim: 1
DRWN   2 Drawing Page(s)
LN.CNT 708
AB     The invention relates to a method of a mass-spectrometric analysis of
       known mutation sites in the genome, such as single nucleotide
       polymorphisms (SNPs), using the method of restricted primer extension.
       The invention consists of the use of primers with a photocleavable
       linker. The linker creates a gap in a DNA strand which is almost the
       same size as a natural DNA building block (nucleoside). The linker forms
       a bridge over a base pair without inhibiting hybridization or enzymatic
       extension. However, the linker allows the primers to be cleaved after
       extension in order to obtain short DNA fragments which can be more
       easily detected on the mass spectrometer.


L5   ANSWER 2 OF 19  USPATFULL
```

09567863

AN 2002:322508 USPATFULL
TI Enhanced secretion of a polypeptide by a microorganism
IN Kolkman, Marc, Oegstgeest, NETHERLANDS
PI US 2002182672 A1 20021205
AI US 2001-975132 A1 20011009 (9)
PRAI US 2000-239531P 20001010 (60)
DT Utility
FS APPLICATION
LREP VICTORIA L. BODY, GENENCOR INTERNATIONAL, INC., 925 PAGE MILL ROAD, PALO ALTO, CA, 94034-1013
CLMN Number of Claims: 52
ECL Exemplary Claim: 1
DRWN 5 Drawing Page(s)
LN.CNT 1405
AB Described herein are methods for the enhanced production of secreted proteins. The secretion of a protein of interest having a substantially non-polar carboxy tail is enhanced by the placement of charged amino acid residues at the carboxy terminus either by adding to the native peptide or by replacing, i.e., substituting, the terminal residues of the native peptide.

L5 ANSWER 3 OF 19 USPATFULL
AN 2002:265886 USPATFULL
TI End selection in directed evolution
IN Short, Jay M., Rancho Santa Fe, CA, UNITED STATES
Frey, Gerhard Johann, San Diego, CA, UNITED STATES
PI US 2002146762 A1 20021010
AI US 2001-885551 A1 20010619 (9)
RLI Continuation of Ser. No. US 2000-522289, filed on 9 Mar 2000, PATENTED Continuation-in-part of Ser. No. US 2000-498557, filed on 4 Feb 2000, PENDING Continuation-in-part of Ser. No. US 2000-495052, filed on 31 Jan 2000, PENDING Continuation-in-part of Ser. No. US 1999-332835, filed on 14 Jun 1999, ABANDONED Continuation-in-part of Ser. No. US 1999-276860, filed on 26 Mar 1999, PATENTED Continuation-in-part of Ser. No. US 1999-267118, filed on 9 Mar 1999, PATENTED Continuation-in-part of Ser. No. US 1999-246178, filed on 4 Feb 1999, PATENTED Continuation-in-part of Ser. No. US 1998-185373, filed on 3 Nov 1998, PATENTED Continuation of Ser. No. US 1996-760489, filed on 5 Dec 1996, PATENTED
PRAI US 1995-8311P 19951207 (60)
DT Utility
FS APPLICATION
LREP GARY CARY WARE & FRIENDENRICH LLP, 4365 EXECUTIVE DRIVE, SUITE 1600, SAN DIEGO, CA, 92121-2189
CLMN Number of Claims: 4
ECL Exemplary Claim: 1
DRWN 7 Drawing Page(s)
LN.CNT 8987
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention provides methods of obtaining novel polynucleotides and encoded polypeptides by the use of non-stochastic methods of directed evolution (DirectEvolution.TM.). A particular advantage of end-selection-based methods is the ability to recover full-length polynucleotides from a library of progeny molecules generated by mutagenesis methods. These methods include non-stochastic polynucleotide site-saturation mutagenesis (Gene Site Saturation Mutagenesis.TM.) and non-stochastic polynucleotide reassembly (GeneReassembly.TM.). This invention provides methods of obtaining novel enzymes that have optimized physical &/or biological properties. Through use of the claimed methods, genetic vaccines, enzymes, small molecules, and other desirable molecules can be evolved towards desirable properties. For example, vaccine vectors, can be obtained that exhibit increased

efficacy for use as genetic vaccines. Vectors obtained by using the methods can have, for example, enhanced antigen expression, increased uptake into a cell, increased stability in a cell, ability to tailor an immune response, and the like. Furthermore, this invention provides methods of obtaining a variety of novel biologically active molecules, in the fields of antibiotics, pharmacotherapeutics, and transgenic traits.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 4 OF 19 USPATFULL
AN 2002:265850 USPATFULL
TI Electrophoretic tag reagents comprising fluorescent compounds
IN Matray, Tracy, San Lorenzo, CA, UNITED STATES
Hernandez, Vincent, Brookdale, CA, UNITED STATES
Singh, Sharat, San Jose, CA, UNITED STATES
PA Aclara BioSciences, Inc. (U.S. corporation)
PI US 2002146726 A1 20021010
AI US 2001-8495 A1 20011109 (10)
RLI Continuation-in-part of Ser. No. US 2000-698846, filed on 27 Oct 2000, PENDING Continuation-in-part of Ser. No. US 2000-602586, filed on 21 Jun 2000, PENDING Continuation-in-part of Ser. No. US 2000-684386, filed on 4 Oct 2000, PENDING Continuation-in-part of Ser. No. US 2000-561579, filed on 28 Apr 2000, ABANDONED Continuation-in-part of Ser. No. US 1999-303029, filed on 30 Apr 1999, GRANTED, Pat. No. US 6322980
DT Utility
FS APPLICATION
LREP PERKINS COIE LLP, P.O. BOX 2168, MENLO PARK, CA, 94026
CLMN Number of Claims: 52
ECL Exemplary Claim: 1
DRWN 7 Drawing Page(s)
LN.CNT 2991
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Electrophoretic probes comprising fluorescent compounds as detection groups and mobility modifiers are disclosed for the multiplexed detection of the binding of, or interaction between, one or more ligands and target antiligands are provided. In one embodiment, detection involves the release of identifying tags as a consequence of target recognition. Target antiligands are contacted with a set of e-tag probes and the contacted antiligands are treated with a selected cleaving agent resulting in a mixture of e-tag reporters. Typically, uncleaved or partially cleaved e-tag probes are removed and the mixture of e-tag reporters is separated by any technique that provides for separation by mass or mass to charge ratio and the like and detected to provide for target identification.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 5 OF 19 USPATFULL
AN 2002:258759 USPATFULL
TI Compositions and methods employing cleavable electrophoretic tag reagents
IN Matray, Tracy, San Lorenzo, CA, UNITED STATES
Hernandez, Vincent, Brookdale, CA, UNITED STATES
Singh, Sharat, San Jose, CA, UNITED STATES
PA Aclara BioSciences, Inc. (U.S. corporation)
PI US 2002142329 A1 20021003
AI US 2001-8573 A1 20011109 (10)
RLI Continuation-in-part of Ser. No. US 2000-698846, filed on 27 Oct 2000, PENDING Continuation-in-part of Ser. No. US 2000-602586, filed on 21 Jun 2000, PENDING Continuation-in-part of Ser. No. US 2000-684386, filed on 4 Oct 2000, PENDING Continuation-in-part of Ser. No. US 2000-561579,

filed on 28 Apr 2000, ABANDONED Continuation-in-part of Ser. No. US 1999-303029, filed on 30 Apr 1999, GRANTED, Pat. No. US 6322980
DT Utility
FS APPLICATION
LREP PERKINS COIE LLP, P.O. BOX 2168, MENLO PARK, CA, 94026
CLMN Number of Claims: 71
ECL Exemplary Claim: 1
DRWN 9 Drawing Page(s)
LN.CNT 3249
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Probe sets for the multiplexed detection of the binding of, or interaction between, one or more ligands and target antiligands are provided. Detection involves the release of identifying tags as a consequence of target recognition. The probe sets include electrophoretic tag probes or e-tag probes, comprising a detection region and a mobility-defining region called the mobility modifier, both linked to a target-binding moiety. Target antiligands are contacted with a set of e-tag probes and the contacted antiligands are treated with a selected cleaving agent resulting in a mixture of e-tag reporters and uncleaved and/or partially cleaved e-tag probes. The mixture is exposed to a capture agent effective to bind to uncleaved or partially cleaved e-tag probes, followed by electrophoretic separation. In a multiplexed assay, different released e-tag reporters may be separated and detected providing for target identification. The methods employ compositions comprising luminescent molecules such as, for example, fluorescent molecules, which are modified to provide for electrophoretic properties that differ for each modified luminescent molecule while maintaining substantially the same absorption, emission and quantum yield properties of the original luminescent molecule. The compositions may be cleavably linked to binding molecules to form the e-tag probes.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 6 OF 19 USPATFULL
AN 2002:243051 USPATFULL
TI Compositions and methods for the therapy and diagnosis of ovarian cancer
IN Algate, Paul A., Issaquah, WA, UNITED STATES
Jones, Robert, Seattle, WA, UNITED STATES
Harlocker, Susan L., Seattle, WA, UNITED STATES
PA Corixa Corporation, Seattle, WA, UNITED STATES, 98104 (U.S. corporation)
PI US 2002132237 A1 20020919
AI US 2001-867701 A1 20010529 (9)
PRAI US 2000-207484P 20000526 (60)
DT Utility
FS APPLICATION
LREP SEED INTELLECTUAL PROPERTY LAW GROUP PLLC, 701 FIFTH AVE, SUITE 6300, SEATTLE, WA, 98104-7092
CLMN Number of Claims: 11
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 25718
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Compositions and methods for the therapy and diagnosis of cancer, particularly ovarian cancer, are disclosed. Illustrative compositions comprise one or more ovarian tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly ovarian cancer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 7 OF 19 USPATFULL
AN 2002:171867 USPATFULL
TI Sets of generalized target-binding e-tag probes
IN Singh, Sharat, San Jose, CA, UNITED STATES
Matray, Tracy, San Lorenzo, CA, UNITED STATES
Chenna, Ahmed, Sunnyvale, CA, UNITED STATES
PI US 2002090616 A1 20020711
AI US 2001-825244 A1 20010402 (9)
RLI Continuation of Ser. No. US 1999-303029, filed on 30 Apr 1999, GRANTED, Pat. No. US 6322980 Continuation of Ser. No. US 2000-561579, filed on 28 Apr 2000, ABANDONED Continuation of Ser. No. US 2000-602586, filed on 21 Jun 2000, PENDING Continuation of Ser. No. US 2000-684386, filed on 4 Oct 2000, PENDING Continuation of Ser. No. US 2000-698846, filed on 27 Oct 2000, PENDING
DT Utility
FS APPLICATION
LREP PERKINS COIE LLP, P.O. BOX 2168, MENLO PARK, CA, 94026
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN 45 Drawing Page(s)
LN.CNT 4208
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Probe sets for the multiplexed detection of the binding of, or interaction between, one or more ligands and target antiligands are provided. Detection involves the release of identifying tags as a consequence of target recognition. The probe sets include electrophoretic tag probes or e-tag probes, comprising a detection region and a mobility-defining region called the mobility modifier, both linked to a target-binding moiety. Target antiligands are contacted with a set of e-tag probes and the contacted antiligands are treated with a selected cleaving agent resulting in a mixture of e-tag reporters and uncleaved and/or partially cleaved e-tag probes. The mixture is exposed to a capture agent effective to bind to uncleaved or partially cleaved e-tag probes, followed by electrophoretic separation. In a multiplexed assay, different released e-tag reporters may be separated and detected providing for target identification.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 8 OF 19 USPATFULL
AN 2002:112528 USPATFULL
TI Generalized target-binding e-tag probe compositions
IN Singh, Sharat, San Jose, CA, UNITED STATES
Salimi-Moosavi, Hossein, Sunnyvale, CA, UNITED STATES
Xiao, Vivian, Cupertino, CA, UNITED STATES
PI US 2002058263 A1 20020516
AI US 2001-824861 A1 20010402 (9)
RLI Continuation of Ser. No. US 1999-303029, filed on 30 Apr 1999, UNKNOWN
DT Utility
FS APPLICATION
LREP IOTA PI LAW GROUP, 350 CAMBRIDGE AVENUE SUITE 250, P O BOX 60850, PALO ALTO, CA, 94306-0850
CLMN Number of Claims: 4
ECL Exemplary Claim: 1
DRWN 45 Drawing Page(s)
LN.CNT 4113
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Compositions for the multiplexed detection of the binding of, or interaction between, one or more ligands and target antiligands are provided. The compositions include one or more uncleaved or partially cleaved electrophoretic tag (e-tag) probes from a set of e-tag probes,

at least one e-tag reporter out of a possible set of e-tag reporters and a capture agent. Detection involves the release of identifying tags as a consequence of target recognition. The e-tag probes comprise a detection region and a mobility-defining region called the mobility modifier, both linked to a target-binding moiety. Target antiligands are contacted with a set of e-tag probes and the contacted antiligands are treated with a selected cleaving agent resulting in a mixture of e-tag reporters and uncleaved and/or partially cleaved e-tag probes. The mixture is exposed to a capture agent effective to bind to uncleaved or partially cleaved e-tag probes, followed by electrophoretic separation. In a multiplexed assay, different released e-tag reporters may be separated and detected providing for target identification.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 9 OF 19 USPATFULL
AN 2002:85692 USPATFULL
TI Oligonucleotide-binding e-tag probe compositions
IN Singh, Sharat, San Jose, CA, UNITED STATES
Tian, Huan, Los Altos, CA, UNITED STATES
PI US 2002045738 A1 20020418
AI US 2001-825245 A1 20010402 (9)
RLI Continuation of Ser. No. US 1999-303029, filed on 30 Apr 1999, PENDING
Continuation of Ser. No. US 2000-561579, filed on 28 Apr 2000, PENDING
Continuation of Ser. No. US 2000-602586, filed on 21 Jun 2000, PENDING
Continuation of Ser. No. US 2000-684386, filed on 4 Oct 2000, PENDING
Continuation of Ser. No. US 2000-698846, filed on 27 Oct 2000, PENDING
DT Utility
FS APPLICATION
LREP IOTA PI LAW GROUP, 350 CAMBRIDGE AVENUE SUITE 250, P O BOX 60850, PALO ALTO, CA, 94306-0850
CLMN Number of Claims: 19
ECL Exemplary Claim: 1
DRWN 45 Drawing Page(s)
LN.CNT 4184
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Compositions for the multiplexed detection of known, selected nucleotide target sequences are provided. The compositions include one or more uncleaved or partially cleaved electrophoretic tag (e-tag) probes from a set of e-tag probes, at least one e-tag reporter out of a possible set of e-tag reporters and a capture agent. The e-tag probes comprise a detection region and a mobility-defining region called the mobility modifier, both linked to a target-binding moiety. Detection involves the release of identifying tags as a consequence of target recognition. The target-binding moiety of the e-tag probes hybridizes to complementary target sequences followed by nuclease cleavage of the e-tag probes and release of detectable e-tags or e-tag reporters. The mixture is exposed to a capture agent which binds uncleaved and/or partially cleaved e-tag probes, followed by electrophoretic separation. In a multiplexed assay, different released e-tag reporters may be separated and detected providing for target identification.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 10 OF 19 USPATFULL
AN 2002:27108 USPATFULL
TI Sets of oligonucleotide-binding e-tag probes
IN Singh, Sharat, San Jose, CA, UNITED STATES
Matray, Tracy, San Lorenzo, CA, UNITED STATES
Chenna, Ahmed, Sunnyvale, CA, UNITED STATES
PI US 2002015954 A1 20020207
AI US 2001-825246 A1 20010402 (9)

09567863

RLI Continuation of Ser. No. US 1999-303029, filed on 30 Apr 1999, PENDING
Continuation of Ser. No. US 2000-561579, filed on 28 Apr 2000, PENDING
Continuation of Ser. No. US 2000-602586, filed on 21 Jun 2000, PENDING
Continuation of Ser. No. US 2000-684386, filed on 4 Oct 2000, PENDING
Continuation of Ser. No. US 2000-698846, filed on 27 Oct 2000, PENDING
DT Utility
FS APPLICATION
LREP IOTA PI LAW GROUP, 350 CAMBRIDGE AVENUE SUITE 250, P O BOX 60850, PALO ALTO, CA, 94306-0850
CLMN Number of Claims: 15
ECL Exemplary Claim: 1
DRWN 45 Drawing Page(s)
LN.CNT 4140
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Probe sets for the multiplexed detection of known, selected nucleotide target sequences are provided. Detection involves the release of identifying tags as a consequence of target recognition. The probe sets include electrophoretic tag probes or "e-tag probes", comprising a detection region and a mobility-defining region called the mobility modifier, both linked to a target-binding moiety. The target-binding moiety of the e-tag probes hybridizes to complementary target sequences followed by nuclease cleavage of the e-tag probes and release of detectable e-tags or e-tag reporters. The mixture is exposed to a capture agent which binds uncleaved and/or partially cleaved e-tag probes, followed by electrophoretic separation. In a multiplexed assay, different released e-tag reporters may be separated and detected providing for target identification.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 11 OF 19 USPATFULL
AN 2002:16857 USPATFULL
TI Kits employing oligonucleotide-binding e-tag probes
IN Singh, Sharat, San Jose, CA, UNITED STATES
Matray, Tracy, San Lorenzo, CA, UNITED STATES
Chenna, Ahmed, Sunnyvale, CA, UNITED STATES
PI US 2002009737 A1 20020124
AI US 2001-824905 A1 20010402 (9)
RLI Continuation of Ser. No. US 1999-303029, filed on 30 Apr 1999, PENDING
Continuation of Ser. No. US 2000-561579, filed on 28 Apr 2000, PENDING
Continuation of Ser. No. US 2000-602586, filed on 21 Jun 2000, PENDING
Continuation of Ser. No. US 2000-684386, filed on 4 Oct 2000, PENDING
Continuation of Ser. No. US 2000-698846, filed on 27 Oct 2000, PENDING
DT Utility
FS APPLICATION
LREP Iota Pi Law Group, P.O. Box 60850, Palo Alto, CA, 94306-0850
CLMN Number of Claims: 10
ECL Exemplary Claim: 1
DRWN 45 Drawing Page(s)
LN.CNT 4157
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Kits for the multiplexed detection of known, selected nucleotide target sequences are provided. Detection involves the release of identifying tags as a consequence of target recognition. The kits include sets of electrophoretic tag probes or e-tag probes, capture agent and optionally a nuclease. The e-tag probes comprise a detection region and a mobility-defining region called the mobility modifier, both linked to a target-binding moiety. In using the kits, the target-binding moiety of the e-tag probes hybridizes to complementary target sequences followed by nuclease cleavage of the e-tag probes and release of detectable e-tags or e-tag reporters. The mixture is exposed to a capture agent which binds uncleaved and/or partially cleaved e-tag probes, followed by

electrophoretic separation. In a multiplexed assay, different released e-tag reporters may be separated and detected providing for target identification.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 12 OF 19 USPATFULL
AN 2002:3833 USPATFULL
TI Methods employing oligonucleotide-binding e-tag probes
IN Singh, Sharat, San Jose, CA, UNITED STATES
Tian, Huan, Los Altos, CA, UNITED STATES
PI US 2002001808 A1 20020103
AI US 2001-825247 A1 20010402 (9)
RLI Continuation of Ser. No. US 1999-303029, filed on 30 Apr 1999, PENDING
Continuation of Ser. No. US 2000-561579, filed on 28 Apr 2000, PENDING
Continuation of Ser. No. US 2000-602586, filed on 21 Jun 2000, PENDING
Continuation of Ser. No. US 2000-684386, filed on 4 Oct 2000, PENDING
Continuation of Ser. No. US 2000-698846, filed on 27 Oct 2000, PENDING
DT Utility
FS APPLICATION
LREP IOTA PI LAW GROUP, 350 CAMBRIDGE AVENUE SUITE 250, P O BOX 60850, PALO ALTO, CA, 94306-0850
CLMN Number of Claims: 10
ECL Exemplary Claim: 1
DRWN 45 Drawing Page(s)
LN.CNT 4155
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods for the multiplexed detection of known, selected nucleotide target sequences are provided. Detection involves the release of identifying tags as a consequence of target recognition. The methods include the use of electrophoretic tag probes or e-tag probes, comprising a detection region and a mobility-defining region called the mobility modifier, both linked to a target-binding moiety. In practicing the methods, the target-binding moiety of the e-tag probes hybridizes to complementary target sequences followed by nuclease cleavage of the e-tag probes and release of detectable e-tags or e-tag reporters. The mixture is exposed to a capture agent which binds uncleaved and/or partially cleaved e-tag probes, followed by electrophoretic separation. In a multiplexed assay, different released e-tag reporters may be separated and detected providing for target identification.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 13 OF 19 USPATFULL
AN 2002:297432 USPATFULL
TI Non-stochastic generation of genetic vaccines
IN Short, Jay M., Rancho Santa Fe, CA, United States
PA Diversa Corporation, San Diego, CA, United States (U.S. corporation)
PI US 6479258 B1 20021112
AI US 2000-495052 20000131 (9)
RLI Continuation-in-part of Ser. No. US 1999-276860, filed on 26 Mar 1999
Continuation-in-part of Ser. No. US 1999-246178, filed on 4 Feb 1999, now patented, Pat. No. US 6171820 Continuation-in-part of Ser. No. US 1998-185373, filed on 3 Nov 1998 Continuation-in-part of Ser. No. US 1996-760489, filed on 5 Dec 1996, now patented, Pat. No. US 5830696
PRAI US 1995-8311P 19951207 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Park, Hankyel T.
LREP Gray Cary Ware & Freidenrich LLP, Haile, Lisa A.
CLMN Number of Claims: 86
ECL Exemplary Claim: 1

09567863

DRWN 66 Drawing Figure(s); 61 Drawing Page(s)
LN.CNT 19213
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention provides methods of obtaining vaccines by use of non-stochastic methods of directed evolution (DirectEvolution.TM.). These methods include non-stochastic polynucleotide site-satuaration mutagenesis (Gene Site Saturation Mutagenesis.TM.) and non-stochastic polynucleotide reassembly (GeneReassembly.TM.). Through use of the claimed methods, vectors can be obtained which exhibit increased efficacy for use as genetic vaccines. Vectors obtained by using the methods can have, for example, enhanced antigen expression, increased uptake into a cell, increased stability in a cell, ability to tailor an immune response, and the like.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 14 OF 19 USPATFULL
AN 2002:63712 USPATFULL
TI Exonuclease-mediated **nucleic acid** reassembly in directed evolution
IN Short, Jay M., Rancho Santa Fe, CA, United States
Djavakhishvili, Tsotne David, San Diego, CA, United States
Frey, Gerhard Johann, San Diego, CA, United States
PA Diversa Corporation, San Diego, CA, United States (U.S. corporation)
PI US 6361974 B1 20020326
AI US 2000-535754 20000327 (9)
RLI Continuation-in-part of Ser. No. US 2000-522289, filed on 9 Mar 2000
Continuation-in-part of Ser. No. US 2000-498557, filed on 4 Feb 2000
Continuation-in-part of Ser. No. US 2000-495052, filed on 31 Jan 2000
Continuation-in-part of Ser. No. US 1999-332835, filed on 14 Jun 1999
Continuation-in-part of Ser. No. US 1999-276860, filed on 26 Mar 1999
Continuation-in-part of Ser. No. US 1999-267118, filed on 9 Mar 1999
Continuation-in-part of Ser. No. US 1999-246178, filed on 4 Feb 1999
Continuation-in-part of Ser. No. US 1998-185373, filed on 3 Nov 1998
Continuation of Ser. No. US 1996-760489, filed on 5 Dec 1996, now patented, Pat. No. US 5830696 Continuation-in-part of Ser. No. US 1997-962504, filed on 31 Oct 1997, now patented, Pat. No. US 6029056 Continuation-in-part of Ser. No. US 1996-677112, filed on 9 Jul 1996, now patented, Pat. No. US 5965408 Continuation-in-part of Ser. No. US 1996-651568, filed on 22 May 1996, now patented, Pat. No. US 5939250
PRAI US 1995-8311P 19951207 (60)
US 1995-8316P 19951207 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Park, Hankyel T.
LREP Gray Cary Ware & Freidenrich, Haile, Lisa A., Shen, Greg
CLMN Number of Claims: 15
ECL Exemplary Claim: 1
DRWN 6 Drawing Figure(s); 6 Drawing Page(s)
LN.CNT 7313
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention provides methods of obtaining novel polynucleotides and encoded polypeptides by the use of non-stochastic methods of directed evolution (DirectEvolution.TM.). A particular advantage of exonuclease-mediated reassembly methods is the ability to reassemble **nucleic acid** strands that would otherwise be problematic to chimerize. Exonuclease-mediated reassembly methods can be used in combination with other mutagenesis methods provided herein. These methods include non-stochastic polynucleotide site-saturation mutagenesis (Gene Site Saturation Mutagenesis.TM.) and non-stochastic polynucleotide reassembly (GeneReassembly.TM.). This invention provides methods of obtaining novel enzymes that have optimized physical &/or

biological properties. Through use of the claimed methods, genetic vaccines, enzymes, small molecules, and other desirable molecules can be evolved towards desirable properties. For example, vaccine vectors can be obtained that exhibit increased efficacy for use as genetic vaccines. Vectors obtained by using the methods can have, for example, enhanced antigen expression, increased uptake into a cell, increased stability in a cell, ability to tailor an immune response, and the like. Furthermore, this invention provides methods of obtaining a variety of novel biologically active molecules, in the fields of antibiotics, pharmacotherapeutics, and transgenic traits.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 15 OF 19 USPATFULL
AN 2002:57570 USPATFULL
TI End selection in directed evolution
IN Short, Jay M., Encinitas, CA, United States
Frey, Gerhard Johann, San Diego, CA, United States
PA Diversa Corporation, San Diego, CA, United States (U.S. corporation)
PI US 6358709 B1 20020319
AI US 2000-522289 20000309 (9)
RLI Continuation-in-part of Ser. No. US 2000-498557, filed on 4 Feb 2000 Continuation-in-part of Ser. No. US 2000-495052, filed on 13 Jan 2000 Continuation-in-part of Ser. No. US 1999-332835, filed on 14 Jun 1999, now abandoned Continuation-in-part of Ser. No. US 1999-276860, filed on 26 Mar 1999 Continuation-in-part of Ser. No. US 1999-267118, filed on 9 Mar 1999, now patented, Pat. No. US 6238884 Continuation-in-part of Ser. No. US 1999-246178, filed on 4 Feb 1999, now patented, Pat. No. US 6171820 Continuation-in-part of Ser. No. US 1998-185373, filed on 3 Nov 1998 Continuation of Ser. No. US 1996-760489, filed on 5 Dec 1996, now patented, Pat. No. US 5830696 Continuation-in-part of Ser. No. US 1997-962504, filed on 31 Oct 1997 Continuation-in-part of Ser. No. US 1996-677112, filed on 9 Jul 1996, now patented, Pat. No. US 5965408 Continuation-in-part of Ser. No. US 1996-651568, filed on 22 May 1996, now patented, Pat. No. US 5939250
PRAI US 1995-8311P 19951207 (60)
US 1995-8316P 19951207 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Park, Hankyel T.
LREP Gray Cary Ware & Freidenrich LLP, Haile, Lisa A.
CLMN Number of Claims: 36
ECL Exemplary Claim: 1
DRWN 11 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 7029
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB This invention provides methods of obtaining novel polynucleotides and encoded polypeptides by the use of non-stochastic methods of directed evolution (DirectEvolution.TM.). A particular advantage of end-selection-based methods is the ability to recover full-length polynucleotides from a library of progeny molecules generated by mutagenesis methods. These methods include non-stochastic polynucleotide site-saturation mutagenesis (Gene Site Saturation Mutagenesis.TM.) and non-stochastic polynucleotide reassembly (GeneReassembly.TM.). This invention provides methods of obtaining novel enzymes that have optimized physical &/or biological properties. Through use of the claimed methods, genetic vaccines, enzymes, small molecules, and other desirable molecules can be evolved towards desirable properties. For example, vaccine vectors can be obtained that exhibit increased efficacy for use as genetic vaccines. Vectors obtained by using the methods can have, for example, enhanced antigen expression, increased uptake into a cell, increased stability in a cell, ability to tailor an immune

response, and the like. Furthermore, this invention provides methods of obtaining a variety of novel biologically active molecules, in the fields of antibiotics, pharmacotherapeutics, and transgenic traits.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 16 OF 19 USPATFULL
AN 2001:229389 USPATFULL
TI Kits employing generalized target-binding e-tag probes
IN Singh, Sharat, San Jose, CA, United States
Matray, Tracy, San Lorenzo, CA, United States
Chenna, Ahmed, Sunnyvale, CA, United States
PI US 2001051340 A1 20011213
AI US 2001-824851 A1 20010402 (9)
RLI Continuation of Ser. No. US 1999-303029, filed on 30 Apr 1999, PENDING
Continuation of Ser. No. US 2000-561579, filed on 28 Apr 2000, PENDING
Continuation of Ser. No. US 2000-602586, filed on 21 Jun 2000, PENDING
Continuation of Ser. No. US 2000-684386, filed on 4 Oct 2000, PENDING
Continuation of Ser. No. US 2000-698846, filed on 27 Oct 2000, PENDING
DT Utility
FS APPLICATION
LREP IOTA PI LAW GROUP, 350 CAMBRIDGE AVENUE SUITE 250, P O BOX 60850, PALO ALTO, CA, 94306-0850
CLMN Number of Claims: 4
ECL Exemplary Claim: 1
DRWN 45 Drawing Page(s)
LN.CNT 4110
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Kits for the multiplexed detection of the binding of, or interaction between, one or more ligands and target antiligands are provided. Detection involves the release of identifying tags as a consequence of target recognition. The kits include sets of electrophoretic tag probes or e-tag probes, a capture agent and optionally a cleaving agent. The e-tag probes comprise a detection region and a mobility-defining region called the mobility modifier, both linked to a target-binding moiety. In using the kits, target antiligands are contacted with a set of e-tag probes and the contacted antiligands are treated with a selected cleaving agent resulting in a mixture of e-tag reporters and uncleaved and/or partially cleaved e-tag probes. The mixture is exposed to a capture agent effective to bind to uncleaved or partially cleaved e-tag probes, followed by electrophoretic separation. In a multiplexed assay, different released e-tag reporters may be separated and detected providing for target identification.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 17 OF 19 USPATFULL
AN 2001:223888 USPATFULL
TI Methods employing generalized target-binding e-tag probes
IN Singh, Sharat, San Jose, CA, United States
Salimi-Moosavi, Hossein, Sunnyvale, CA, United States
Xiao, Vivian, Cupertino, CA, United States
PI US 2001049105 A1 20011206
AI US 2001-824984 A1 20010402 (9)
RLI Continuation of Ser. No. US 1999-303029, filed on 30 Apr 1999, PENDING
Continuation of Ser. No. US 2000-561579, filed on 28 Apr 2000, PENDING
Continuation of Ser. No. US 2000-602586, filed on 21 Jun 2000, PENDING
Continuation of Ser. No. US 2000-684386, filed on 4 Oct 2000, PENDING
Continuation of Ser. No. US 2000-698846, filed on 27 Oct 2000, PENDING
DT Utility
FS APPLICATION
LREP IOTA PI LAW GROUP, 350 CAMBRIDGE AVENUE SUITE 250, P O BOX 60850, PALO

09567863

ALTO, CA, 94306-0850
CLMN Number of Claims: 4
ECL Exemplary Claim: 1
DRWN 45 Drawing Page(s)
LN.CNT 4138
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods for the multiplexed detection of the binding of, or interaction between, one or more ligands and target antiligands are provided. Detection involves the release of identifying tags as a consequence of target recognition. The methods include the use of electrophoretic tag probes or e-tag probes, comprising a detection region and a mobility-defining region called the mobility modifier, both linked to a target-binding moiety. In practicing the methods, target antiligands are contacted with a set of e-tag probes and the contacted antiligands are treated with a selected cleaving agent resulting in a mixture of e-tag reporters and uncleaved and/or partially cleaved e-tag probes. The mixture is exposed to a capture agent effective to bind to uncleaved or partially cleaved e-tag probes, followed by electrophoretic separation. In a multiplexed assay, different released e-tag reporters may be separated and detected providing for target identification.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 18 OF 19 USPATFULL
AN 2001:121236 USPATFULL
TI Method of **nucleic acid** analysis
IN Gut, Ivo G., Berlin, Germany, Federal Republic of
Beck, Stephan A., Cambridge, United Kingdom
PA Imperial Cancer Research Technology Limited, London, United Kingdom (non-U.S. corporation)
PI US 6268129 B1 20010731
WO 9627681 19960912
AI US 1997-894836 19971124 (8)
WO 1996-GB476 19960304
19971124 PCT 371 date
19971124 PCT 102(e) date
PRAI GB 1995-4598 19950303
DT Utility
FS GRANTED
EXNAM Primary Examiner: Houtteman, Scott W.
LREP Nixon & Vanderhye P.C.
CLMN Number of Claims: 44
ECL Exemplary Claim: 1
DRWN 31 Drawing Figure(s); 31 Drawing Page(s)
LN.CNT 1990
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method of analysing a **nucleic acid** by mass spectrometry comprising the steps of: (1) preparing a **nucleic acid** molecule comprising a negatively charged non-phosphate sugar-sugar linkage; (2) eliminating the charge from all, or up to all but ten, of the sugar-sugar linkages of the said **nucleic acid** molecule; (3) introducing the said **nucleic acid** molecule in which the charge has been wholly or partly eliminated as said into a mass spectrometer; and (4) determining the mass of the said **nucleic acid** molecule. Preferably, the **nucleic acid** has no or one charge. A method of preparing a **nucleic acid** molecule containing no or up to ten negative charges and no or up to ten positive charges comprising the steps of (1) synthesizing a **nucleic acid** with a phosphorothioate linkage or a phosphoroselenoate linkage between sugar residues, and (2) reacting the said **nucleic acid** with an alkylating agent so as to

eliminate the charge on the said phosphorothioate linkage or said phosphoroselenoate linkage. The methods are useful for DNA sequencing and mutation analysis, and the nucleic acids are useful to suppress gene expression. ##STR1##

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L5 ANSWER 19 OF 19 WPIDS (C) 2002 THOMSON DERWENT
AN 2001-007201 [01] WPIDS
CR 2002-075152 [10]
DNC C2001-001816
TI Detecting a DNA sequence, particularly a single nucleotide polymorphism using a pair of nucleotide sequences, a primer and an snp detection sequence having an electrophoretic tag.
DC B04 D16
IN SINGH, S; SALIMI-MOOSAVI, H; XIAO, V; CHENNA, A; MATRAY, T; TIAN, H
PA (ACLA-N) ACLARA BIOSCIENCES INC; (SALI-I) SALIMI-MOOSAVI H; (SING-I) SINGH S; (XIAO-I) XIAO V; (CHEN-I) CHENNA A; (MATR-I) MATRAY T; (TIAN-I) TIAN H
CYC 93
PI WO 2000066607 A1 20001109 (200101)* EN 76p
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW
AU 2000044972 A 20001117 (200111)
US 6322980 B1 20011127 (200175)
US 2001049105 A1 20011206 (200203)
US 2001051340 A1 20011213 (200204)
US 2002001808 A1 20020103 (200207)
US 2002009737 A1 20020124 (200210)
US 2002015954 A1 20020207 (200213)
EP 1180112 A1 20020220 (200221) EN
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI
US 2002045738 A1 20020418 (200228)
US 2002058263 A1 20020516 (200237)
US 2002090616 A1 20020711 (200248)
ADT WO 2000066607 A1 WO 2000-US11396 20000428; AU 2000044972 A AU 2000-44972 20000428; US 6322980 B1 US 1999-303029 19990430; US 2001049105 A1 Cont of US 1999-303029 19990430, Cont of US 2000-561579 20000428, Cont of US 2000-602586 20000621, Cont of US 2000-684386 20001004, Cont of US 2000-698846 20001027, US 2001-824984 20010402; US 2001051340 A1 Cont of US 1999-303029 19990430, Cont of US 2000-561579 20000428, Cont of US 2000-602586 20000621, Cont of US 2000-684386 20001004, Cont of US 2000-698846 20001027, US 2001-824851 20010402; US 2002001808 A1 Cont of US 1999-303029 19990430, Cont of US 2000-561579 20000428, Cont of US 2000-602586 20000621, Cont of US 2000-684386 20001004, Cont of US 2000-698846 20001027, US 2001-825247 20010402; US 2002009737 A1 Cont of US 1999-303029 19990430, Cont of US 2000-561579 20000428, Cont of US 2000-602586 20000621, Cont of US 2000-684386 20001004, Cont of US 2000-698846 20001027, US 2001-824905 20010402; US 2002015954 A1 Cont of US 1999-303029 19990430, Cont of US 2000-561579 20000428, Cont of US 2000-602586 20000621, Cont of US 2000-684386 20001004, Cont of US 2000-698846 20001027, US 2001-825246 20010402; EP 1180112 A1 EP 2000-926444 20000428, WO 2000-US11396 20000428; US 2002045738 A1 Cont of US 1999-303029 19990430, Cont of US 2000-561579 20000428, Cont of US 2000-602586 20000621, Cont of US 2000-684386 20001004, Cont of US 2000-698846 20001027, US 2001-825245 20010402; US 2002058263 A1 Cont of US 1999-303029 19990430, US 2001-824861 20010402; US 2002090616 A1 Cont of US 1999-303029 19990430, Cont of US 2000-561579 20000428, Cont of US

2000-602586 20000621, Cont of US 2000-684386 20001004, Cont of US 2000-698846 20001027, US 2001-825244 20010402

FDT AU 2000044972 A Based on WO 200066607; EP 1180112 A1 Based on WO 200066607; US 2002090616 A1 Cont of US 6322980

PRAI US 1999-303029 19990430; US 2000-561579 20000428; US 2000-602586 20000621; US 2000-684386 20001004; US 2000-698846 20001027; US 2001-824984 20010402; US 2001-824851 20010402; US 2001-825247 20010402; US 2001-824905 20010402; US 2001-825246 20010402; US 2001-825245 20010402; US 2001-824861 20010402; US 2001-825244 20010402

AN 2001-007201 [01] WPIDS

CR 2002-075152 [10]

AB WO 200066607 A UPAB: 20020730

NOVELTY - DNA sequence in a target **nucleic acid** sample is detected by executing primer extension in the presence of a polymerase, target DNA (TA) and a reagent pair consisting of a primer which specifically binds to TA and detection sequence (DS) comprised of nucleotide bases for each DNA sequence to be determined that binds to TA downstream from primer and has an electrophoretic tag specific for each DNA sequence.

DETAILED DESCRIPTION - The above method (I) comprises:

(a) combining under primer extension conditions, a polymerase having 5' to 3' exonuclease activity, TA and a reagent pair consisting of a primer and DS comprising of nucleotide bases for each DNA sequence to be determined, where each primer specifically binds to TA and DS binds to TA downstream from the primer in the direction of primer extension and has a electrophoretic tag specific for each DNA sequence;

(b) executing at least 1 cycle of the primer extension, where DS bound to target DNA is at least partially degraded with release of the electrophoretic tag free of the detection sequence;

(c) separating released electrophoretic tags into individual fractions; and

(d) detecting the fractions using the tag, where the presence of the DNA sequence in the TA sample is detected, provided that, when separation is performed solely by differences in mass, the electrophoretic tags that are separated all have the same number of nucleotides bonded to the electrophoretic tag.

INDEPENDENT CLAIMS are also included for the following:

(1) determining (II) the amount of at least 1 single nucleotide polymorphism (snp) in a target DNA sample, comprising:

(a) combining with step (a) of (I), a quantitating system comprising at least 2 control sequences having a common primer region and different control detection regions downstream from the primer region in the direction of primer extension, a primer sequence complementary to the primer region and a control DS for each of the control detection regions characterized by having a labeled electrophoretic tag specific for the control DS to which it is bound;

(b) executing at least 1 cycle of primer extension, where snp DS is bound to TA and control DS are partially degraded with release of electrophoretic tags;

(c) electrophoretically separating the tags into separate bands and determining the signal from the label from each of the bands; and

(d) comparing the band signal from control DS with signals from snp DS;

(2) a kit comprising several snp detection sequences characterized by consisting of at least 12 nucleotides, the 5' nucleotide bonded to an electrophoretic tag, the penultimate nucleotide bonded to the adjacent nucleotide by a link resistant to exonuclease hydrolysis and a complementary nucleotide to a snp at other than the terminal nucleotide; and

(3) a kit comprising several compounds of the formula: R-L-T, where R is a fluorescer, L is a linking group selected from NH-lysine,

NH-(lysine)2, NH-alanine, NH-aspartic acid, NH-(aspartic acid)2, NH-(aspartic acid)3, NH-(aspartic acid)4, NH-(aspartic acid)5, NH-(aspartic acid)6, NH-(aspartic acid)7, NH-alanine-lysine, NH-aspartic acid-lysine, NH-(aspartic acid)2-lysine, NH-(aspartic acid)3-lysine, NH-(aspartic acid)4-lysine, NH-(aspartic acid)5-lysine, NH-(aspartic acid)6-lysine, NH-(aspartic acid)7-lysine, NH-(aspartic acid)8-lysine, NH-(lysine)4 and NH-(lysine)5 and T is selected from a purine, pyrimidine, nucleoside, nucleotide, and nucleotide triphosphate.

USE - The method is useful for detecting at least 1 **nucleic acid** sequence or several snps in a target DNA sample.

ADVANTAGE - The method provides an improved analysis of complex **nucleic acid** mixture and for simultaneous identification of several entities such as sequences, snps, alleles, mutations, etc.

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L5 ANSWER 18 OF 19 USPATFULL

TI Method of **nucleic acid** analysis

AB A method of analysing a **nucleic acid** by mass spectrometry comprising the steps of: (1) preparing a **nucleic acid** molecule comprising a negatively charged non-phosphate sugar-sugar linkage; (2) eliminating the charge from all, or up to all but ten, of the sugar-sugar linkages of the said **nucleic acid** molecule; (3) introducing the said **nucleic acid** molecule in which the charge has been wholly or partly eliminated as said into a mass spectrometer; and (4) determining the mass of the said **nucleic acid** molecule. Preferably, the **nucleic acid** has no or one charge. A method of preparing a **nucleic acid** molecule containing no or up to ten negative charges and no or up to ten positive charges comprising the steps of (1) synthesizing a **nucleic acid** with a phosphorothioate linkage or a phosphoroselenoate linkage between sugar residues, and (2) reacting the said **nucleic acid** with an alkylating agent so as to eliminate the charge on the said phosphorothioate linkage or said phosphoroselenoate linkage. The. . .

SUMM To date, a simple and effective method of making **nucleic acid**, particularly DNA, more suitable for analysis by mass spectroscopy, especially when the said **nucleic acid** has been enzymatically synthesised, has not been devised.

SUMM A first aspect of the invention provides a method of analysing a **nucleic acid** by mass spectrometry comprising the steps of (1) providing a **nucleic acid** molecule containing no or up to ten negative charges and no or up to ten positive charges; (2) introducing the said **nucleic acid** molecule into a mass spectrometer; and (3) determining the mass of the said **nucleic acid** molecule, wherein when the **nucleic acid** molecule has no negative charges has greater than 17 sugar-sugar linkages and when the **nucleic acid** has a charge there are fewer charges than there are sugar-sugar linkages.

SUMM Preferably, when the **nucleic acid** has no negative charges it has >20 sugar-sugar linkages; more preferably >30 sugar-sugar linkages; and still more preferably >50 sugar-sugar. . .

SUMM A second aspect of the invention provides a method of analysing a **nucleic acid** by mass spectrometry comprising the steps of (1) preparing a **nucleic acid** molecule comprising a negatively charged non-phosphate sugar-sugar linkage; (2) eliminating the charge from all, or up to all but ten, of the sugar-sugar linkages of the said **nucleic acid** molecule; (3) introducing

the said **nucleic acid** molecule in which the charge has been wholly or partly eliminated as said into a mass spectrometer; and (4) determining the mass of the said **nucleic acid** molecule.

SUMM . . . molecule being analysed such as its relative, rather than its absolute, mass. Therefore, by "determining the mass of the said **nucleic acid** molecule" we include determination of any physical characteristic derivable from the mass or relative mass of the said **nucleic acid** molecule.

SUMM It is preferred if the **nucleic acid** provided in the first aspect of the invention or prepared in the second aspect of the invention has no or. . .

SUMM It is further preferred that the **nucleic acid** is DNA.

SUMM . . . a diester with the said sugar residues. However, as will be clear from the specification we include in the term "**nucleic acid**" (and more particularly in the term DNA) molecules with non-phosphate linkages.

SUMM By the term "**nucleic acid**" we also include molecules with non-natural base analogues; molecules in which the 2' and 3' positions of the pentose sugar. . .

SUMM It is particularly preferred if the **nucleic acid** molecule has no phosphate sugar-sugar linkages.

SUMM It is also preferred if the **nucleic acid** molecule has any of one to ten phosphate sugar-sugar linkages; most preferably one.

SUMM Conveniently, when the **nucleic acid** is uncharged or positively charged, the mass is determined in positive ion mode (PIM); similarly, when the **nucleic acid** is negatively charged, the mass is determined in negative ion mode. Indeed, when the **nucleic acid** molecule is uncharged no signal is detected in NIM.

SUMM The molecular masses of **nucleic acid** molecules as defined in the invention containing from two nucleoside moieties to around 1600 nucleoside moieties can be determined by mass spectroscopy and, as the spectrometers improve, it is envisaged that **nucleic acid** molecules of the invention of greater molecular mass could be used.

SUMM It is most preferred if the **nucleic acid** molecule whose mass is determined has between 2 and 500 nucleoside moieties; preferably between 5 and 300 nucleoside moieties; and. . .

SUMM Conveniently, the mass spectrometer is able to distinguish at least two **nucleic acid** molecules whose mass differs by the mass of a nucleoside moiety.

SUMM Although in some circumstances it may be useful to determine the molecular mass of a single **nucleic acid** species, it is preferred that a plurality of **nucleic acid** molecules with differing molecular mass are introduced into the mass spectrometer and the mass of at least one of the. . .

SUMM As will be discussed in more detail below, it is particularly preferred if the **nucleic acid** is prepared using an enzymatic chain extension step. It is particularly preferred if a polymerase chain reaction or a chain. . .

SUMM The provision of a **nucleic acid** molecule containing no or up to ten negative and no or up to ten positive charges, and the preparation of a **nucleic acid** molecule comprising a negatively charged non-phosphate sugar-sugar linkage, as well as **nucleic acid** molecules which are suitable for use in the methods, are described in the following aspects of the invention.

SUMM It is further preferred if certain salts are removed from the **nucleic acid** before introduction into the mass spectrometer. For example, NaI is produced in some of the methods

described in the third aspect of the invention and it is convenient to remove this salt, and any buffer, from the **nucleic acid**. However, presence of NH.sub.4.sup.+ ions may increase the definition of the MS signal.

SUMM It is still further preferred if the 5' end of any **nucleic acid** is not a free hydroxyl. Preferably, as described below, it may be alkylated. It may also be phosphorylated (for example. . .

SUMM A third aspect of the invention provides a method of preparing a **nucleic acid** molecule containing no or up to ten negative charges and no or up to ten positive charges comprising the steps of (1) synthesising a **nucleic acid** with a phosphorothioate linkage or a phosphoroselenoate linkage between sugar residues, and (2) reacting the said **nucleic acid** with an alkylating agent so as to eliminate the charge on the said phosphorothioate linkage or said phosphoroselenoate linkage.

SUMM A particular advantage of this method is that uncharged, or substantially uncharged, **nucleic acid** can be made post-synthetically. A further advantage is that uncharged, or substantially uncharged, **nucleic acid** can be made which is longer than any uncharged **nucleic acid** that has been (or can be) made by de novo chemical synthesis.

SUMM Preferably the **nucleic acid** is DNA. Conveniently the **nucleic acid** molecule with a phosphorothioate linkage or with a phosphoroselenoate linkage is synthesised chemically, for example using solid phase phosphoramidite chemistry.. . .

SUMM Alternatively, the **nucleic acid** molecule with a phosphorothioate linkage or with a phosphoroselenoate linkage is synthesised enzymatically. In this embodiment, an .alpha.S-dNTP or an .alpha.Se-dNTP is incorporated into a growing **nucleic acid** chain using a polymerase enzyme. At least the .alpha.S-dNTPs are readily commercially available for example from United States Biochemical Corporation,. . .

SUMM The Klenow fragment of E. coli DNA polymerase is a preferred enzyme and in this embodiment a **nucleic acid** template and a primer are used to synthesise the **nucleic acid** molecule. Conveniently, the primer is an oligonucleotide wherein each of the sugar-sugar linkages is either a phosphorothioate or a phosphoroselenoate. . .

SUMM . . . is preferred if step (1) of the method of the third aspect of the invention further comprises (a) synthesising said **nucleic acid** with a taggable group, said taggable group being capable of accepting a positive charge either directly or indirectly either before or after step (2), or (b) synthesising said **nucleic acid** with a precursor that comprises a positively charged moiety.

SUMM It is preferred if the **taggable** group accepts the **positive charge** before step (2).

SUMM . . . or can be made positively charged. By "indirectly" we mean that there is a linker (ie chemical spacer) between the **taggable** group and the **positive charge**.

SUMM . . . more detail in Example 5, amino (or ammonium) groups, more particularly quaternary ammonium tags, may usefully be added to the **nucleic acid** that is to be analysed by mass-spectrometry. Suitably, the amino (or ammonium) group is added to a synthetic oligonucleotide (such. . . positively charged group (which is preferably a quaternary ammonium-containing compound) is then attached to the aliphatic --NH.sub.2 group in the **nucleic acid**. Conveniently, the quaternary ammonium-containing compound comprises hydroxysuccinimidyl ester which reacts with aliphatic --NH.sub.2 groups; preferably the compound is trimethyl ammonium. . .

SUMM The precursor of the **nucleic acid** may be any suitable precursor which comprises a positively-charged moiety. It is

particularly preferred if the precursor is a dideoxynucleotide comprising a positively charged moiety and that the precursor is introduced into the **nucleic acid** using a polymerase. Conveniently, the dideoxynucleotide comprising a positively charged moiety is made from a nucleotide precursor that comprises an aliphatic amino group. Suitably, the dideoxynucleotide comprising a positively charged moiety is introduced into the **nucleic acid** in a Sanger sequencing reaction.

SUMM It is preferred if substantially all of the negative charges of the **nucleic acid** are removed and a single positive charge remains on the **nucleic acid** molecule.

SUMM In one preferred embodiment, as well as an .alpha.S-dNTP or an .alpha.Se-dNTP being incorporated in a growing **nucleic acid** chain using a polymerase enzyme, a chain terminating a nucleotide is used in order to terminate the chain. Suitable chain. . .

SUMM . . . .alpha.S-dNTP or .alpha.Se-dNTP (or a mixture thereof) in the presence of .alpha.S-ddNTP or .alpha.Se-ddNTP will lead to a plurality of **nucleic acid** molecules of varying sizes in which all of the sugar-sugar linkages are either a phosphorothioate linkage or a phosphoroselenoate linkage,. . . reacting with an alkylating agent so as to eliminate the charge on the said linkage. Thus, in this embodiment a **nucleic acid** molecule with no charge is produced.

SUMM . . . has each sugar-sugar linkage as a phosphorothioate or phosphoroselenoate linkage, and either .alpha.S-dNTP or .alpha.Se-dNTP is used to extend the **nucleic acid** chain, then incorporation of a ddNTP will yield a **nucleic acid** molecule wherein the 3'-most sugar-sugar linkage is a phosphate linkage, and all other sugar-sugar linkages are either phosphorothioate or phosphoroselenoate.. . .

SUMM . . . atom or phosphoroselenoate Se atom. Thus, it is preferred if the alkylating agent does not react with the bases of **nucleic acid** or with any free hydroxyl groups of the **nucleic acid**.

SUMM . . . completely with the phosphorothioate S atom or phosphoroselenoate Se atom and substantially completely with other reactive groups in the said **nucleic acid**, for example the bases of the **nucleic acid** or any free hydroxyl group of the **nucleic acid**.

SUMM . . . case, it is preferred if the alkylating agent is substantially incapable of alkylating a phosphate group to form a stable **nucleic acid**.

SUMM When the alkylated **nucleic acid** molecule of this third aspect of the invention is analysed using the first or second aspects of the invention it. . . Thus, it is particularly preferred that substantially all phosphorothioate linkages or substantially all phosphoroselenoate linkages of substantially all of the **nucleic acid** molecules are so alkylated. It does not matter if other reactive groups of the **nucleic acid** molecule (such as the bases or hydroxyl groups) so long as that alkylation is substantially complete and to the same. . .

SUMM . . . is important so that the masses or mass differences detected reflect differences in the number of nucleoside moieties in a **nucleic acid** molecule rather than the extent of alkylation.

SUMM . . . more detail in the Examples, the mass of each (or at least a substantial number) of the plurality of the **nucleic acid** molecules so generated can be determined according to the first or second aspect of the invention and, because the mass. . . difference expected for each nucleoside moiety (comprising a base A, G, C or T) is known, the sequence of a **nucleic acid** can

be determined.

SUMM . . . the invention) can be used to determine mutations in a DNA sequence. Thus, for example, the mass of a given **nucleic acid** sequence can be readily calculated from the known molecular masses of bases, sugar and sugar-sugar linkages. If one or more bases is replaced by another base (as occurs in a mutation), the mass of the said given **nucleic acid** sequence will change in a predictable way. Thus, as is apparent (and is described in more details in the Examples). . .

SUMM In this embodiment of the invention it is particularly preferred if the **nucleic acid** molecule with a given sequence is produced by a polymerase chain reaction. The primers used in the PCR may be. . .

SUMM . . . the primers contain no phosphate linkage. The sequence of the primers are designed using well established principles so that the **nucleic acid** sequence of interest is amplified. Conveniently, .alpha.S-dNTPs or .alpha.Se-dNTPs are used and the resulting DNA molecule has only either phosphorothioate. . .

SUMM A fourth aspect of the invention provides a method of preparing a **nucleic acid** molecule containing no or up to ten negative charges comprising the steps of synthesising enzymatically the said **nucleic acid** using a dNTP uncharged at least at the .alpha.-phosphorus position.

SUMM Conveniently, the **nucleic acid** is synthesised using a primer and a polymerase.

SUMM As described in relation to the third aspect of the invention, various **nucleic acid** molecules are suitable as primers. It is preferred if the primer is an oligonucleotide wherein each of the sugar-sugar linkages. . .

SUMM A fifth aspect of the invention provides an uncharged **nucleic acid** molecule has greater than 17 sugar-sugar linkages. Preferably, the **nucleic acid** molecule has >20; more preferably >30 and still more preferably >50 sugar-sugar linkages. Such molecules are readily synthesised using, for. . .

SUMM A sixth aspect of the invention provides a **nucleic acid** molecule with no or up to ten negative charges wherein at least one sugar-sugar linkage comprises an alkylated phosphorothioate moiety. . .

SUMM A seventh aspect of the invention provides an uncharged **nucleic acid** molecule comprising a phosphoro sugar-sugar linkage wherein in each phosphoro linkage the phosphorous atom is substituted with any one of. . .

SUMM An eighth aspect of the invention provides a **nucleic acid** molecule containing one to ten phosphate sugar-sugar linkages wherein all other sugar-sugar linkages are uncharged. Preferably the **nucleic acid** comprises at least 20 nucleoside residues; more preferably at least 50 nucleoside residues.

SUMM A further aspect of the invention provides a **nucleic acid** with one or up to ten positive charges wherein the sugar-sugar linkages are uncharged. Preferably, each sugar-sugar linkage is either an, alkylated phosphorothioate moiety or an alkylated phosphoroselenoate moiety. More preferably the **nucleic acid** has a single positive charge. The nucleic acids of this aspect of the invention can be synthesised using a method. . .

SUMM . . . completely with the phosphorothioate S atom or phosphoroselenoate Se atom and substantially completely with other reactive groups in the said **nucleic acid** molecule.

SUMM Preferably the use to which the alkylating agent is put is to alkylate a **nucleic acid** wherein each of the sugar-sugar linkages is either a phosphorothioate or a phosphoroselenoate linkage; or wherein up to ten sugar-sugar. . .

SUMM . . . of the invention provide a method of suppressing gene

expression in a cell comprising administering to the cell an antisense **nucleic acid** wherein the antisense **nucleic acid** is a **nucleic acid** obtainable by the third and fourth aspects of the invention or a **nucleic acid** of the fifth, sixth, seventh or eighth aspects of the invention; use of any of the said nucleic acids as an antisense **nucleic acid**; a said **nucleic acid** for use in medicine; and a pharmaceutical formulation comprising a said **nucleic acid** and a pharmaceutically acceptable carrier.

SUMM It is particularly preferred that the **nucleic acid** is the **nucleic acid** obtainable by the method of the third aspect of the invention, in particular by synthesising a **nucleic acid** with a phosphorothioate linkage between sugar residues and reacting the said **nucleic acid** with an alkylating agent so as to eliminate the charge on the said phosphorothioate linkage.

SUMM . . . (more usually referred to as antisense oligonucleotides although we do not use this to indicate a size limitation) are single-stranded **nucleic acid**, which can specifically bind to a complementary **nucleic acid** sequence. By binding to the appropriate target sequence, an RNA-RNA, a DNA-DNA, or RNA-DNA duplex is formed. These nucleic acids. . . could recognise sequences in the major groove of the DNA double helix. A triple helix was formed thereby. Thus, the **nucleic acid** molecules of the invention may be able to specifically bind double-stranded DNA via recognition of major groove hydrogen binding sites.

SUMM By binding to the target **nucleic acid**, the above oligonucleotides can inhibit the function of the target **nucleic acid**. This is, for example, a result of blocking the transcription, processing, poly(A) addition. replication, translation, or promoting inhibitory mechanisms of. . .

SUMM . . . HL60, which over expresses the c-myc proto-oncogene. The antisense oligonucleotide used was complementary to regions of the c-myc mRNA. A **nucleic acid** of the present invention with the same base sequence is expected to work in the same way with an advantage. . .

SUMM Antisense oligonucleotides can also be used to inhibit replication and expression of **nucleic acid** foreign to the host cells. The antisense oligonucleotides are prepared as described above and then introduced into cells, for example. . .

SUMM . . . amount. The local high concentration of oligonucleotides enhances penetration of the targeted cells and effectively blocks translation of the target **nucleic acid** sequences.

SUMM A still further aspect of the invention provides a method of analysing a **nucleic acid** by mass spectrometry comprising the steps of (1) providing a **nucleic acid** molecule comprising a positively-charged moiety; (2) introducing the said **nucleic acid** molecule into a mass spectrometer; and (3) determining the mass of the said **nucleic acid**. Preferably the sugar-sugar linkages of the **nucleic acid** are substantially all phosphate sugar-sugar linkages. As is shown in Example 5, there are advantages to including a positively charged moiety into a **nucleic acid** whether or not the negative charges of the sugar-sugar linkages are eliminated or not.

SUMM A further aspect of the invention provides a method of preparing a **nucleic acid** comprising a positively-charged moiety comprising synthesising a **nucleic acid** with a taggable group, said taggable group being capable of accepting a positive charge either directly or indirectly. Preferably, the sugar-sugar linkages of the **nucleic acid** are substantially all phosphate sugar-sugar linkages.

SUMM . . . or can be made positively charged. By "indirectly" we mean that there is a linker (ie chemical spacer) between the **taggable** group and the **positive charge**.

SUMM . . . more detail in Example 5, amino (or ammonium) groups, more particularly quaternary ammonium tags, may usefully be added to the **nucleic acid** that is to be analysed by mass-spectrometry. Suitably, the amino (or ammonium) group is added to a synthetic oligonucleotide (such. . . positively charged group (which is preferably a quaternary ammonium-containing compound) is then attached to the aliphatic --NH.sub.2 group in the **nucleic acid**. Conveniently, the quaternary ammonium-containing compound comprises hydroxysuccinimidyl ester which reacts with aliphatic --NH.sub.2 groups; preferably the compound is trimethyl ammonium. . .

DETD . . . efficient and clean. The combination of these two reactions is very simple. No side products were observed. Attaching a single **positive charge** via a **charge tag** has the advantage that there is no need for a high acidity in the matrix which leads to degradation of. . .

CLM What is claimed is:

1. A method of analyzing a **nucleic acid** by mass spectrometry comprising the steps of (1) providing a positively charged or negatively charged **nucleic acid** molecule containing one or up to ten negative charges and no or up to ten positive charges, or no negative charges and one or up to ten positive charges, wherein the **nucleic acid** molecule has a sugar-linkage-sugar backbone and said sugars have a base attached thereto at the 1 position; and there are fewer negative charges than there are sugar-sugar linkages; (2) introducing the said **nucleic acid** molecule into a mass spectrometer; and (3) determining the mass of the said **nucleic acid** molecule.

2. A method of analyzing a **nucleic acid** by mass spectrometry wherein the **nucleic acid** molecule has a sugar-linkage-sugar backbone and said sugars have a base attached thereto at the 1 position; said method comprising the steps of (1) preparing a **nucleic acid** molecule comprising a negatively charged non-phosphate sugar-sugar linkage; (2) eliminating charge from the sugar-sugar linkages of the said **nucleic acid** molecule by covalent modification of the negatively charged non-phosphate sugar-sugar linkage so that the resulting **nucleic acid** molecule is positively charged or negatively charged and said molecule contains one or up to ten negative charges, being fewer charges than there are sugar-sugar linkages; (3) introducing the said **nucleic acid** molecule in which the charge has been partly eliminated as said into a mass spectrometer; and (4) determining the mass of the said **nucleic acid** molecule.

3. A method according to claim 2 wherein the said **nucleic acid** molecule has one phosphate sugar-sugar linkage.

4. A method according to claim 1 wherein the **nucleic acid** has one charge.

5. A method according to claim 1 wherein the **nucleic acid** DNA or an analouge or derivative thereof wherein the sugar residue comprises a 2'-deoxyribose.

7. A method according to claim 1 wherein when the **nucleic acid** is uncharged or positively charged the mass is determined by detection in positive ion mode.

8. A method according to claim 1 wherein when the **nucleic**

acid is negatively charged the mass is determined by detection in negative ion mode.

9. A method according to claim 1 wherein a plurality of **nucleic acid** molecules with differing molecular mass are introduced into the mass spectrometer and the mass of at least one of the. . . . . 10. A method according to claim 1 wherein an enzymatic chain extension step is used in the preparation of the **nucleic acid**.

. . . A method according to claim 9 wherein a polymerase chain reaction is used in the preparation of the plurality of **nucleic acid** molecules.

12. A method according to claim 9 wherein a **nucleic acid** chain terminating reagent is used in the preparation of the plurality of nucleic acids.

. . . step of determining a nucleotide sequence or detecting a mutation by comparing the mass differences of the said plurality of **nucleic acid** molecules.

14. A method of preparing a **nucleic acid** molecule containing no or up to ten negative charges or a **nucleic acid** molecule containing no or up to ten positive charges wherein the **nucleic acid** molecule has a sugar-linkage-sugar backbone and said sugars have a base attached thereto at the 1 position; said method comprising the steps of (1) synthesizing a **nucleic acid** with a phosphorothioate linkage or a phosphoroselenoate linkage between sugar residues, and (2) reacting the said **nucleic acid** with an alkylating agent so as to eliminate the charge on the said phosphorothioate linkage or said phosphoroselenoate linkage wherein step (1) further comprises (a) synthesizing said **nucleic acid** with a taggable group, said taggable group being capable of accepting a positive charge either directly or indirectly and either before or after step (2), or (b) synthesizing said **nucleic acid** with a precursor that comprises a positively charged moiety.

15. A method of preparing a positively charged or negatively charged **nucleic acid** molecule containing one or up to ten negative charges and no or up to ten positive charges or no negative charges and one or up to ten positive charges, said **nucleic acid** molecule comprising a sugar-linkage-sugar backbone wherein said sugars have a base attached thereto at the 1 position; said method comprising the steps of (1) enzymatically synthesizing a **nucleic acid** with a phosphorothioate linkage or a phosphoroselenoate linkage between sugar residues, and (2) reacting the said **nucleic acid** with an alkylating agent so as to eliminate the charge on the said phosphorothioate linkage or said phosphoroselenoate linkage, wherein said **nucleic acid** molecule consists of at least 4 nucleoside moieties.

16. A method of analyzing a **nucleic acid** by mass spectrometry comprising the steps of (1) providing a positively or negatively charged **nucleic acid** molecule obtainable by the method of claim 15, containing one or up to ten negative charges and no or up. . . up to ten positive charges, wherein there are fewer negative charges than there are sugar-sugar linkages; (2) introducing the said **nucleic acid** molecule into a mass spectrometer; and (3) determining the mass of the said **nucleic acid** molecule.

17. A method according to claim 14 wherein the **nucleic acid** with a phosphorothioate linkage or a phosphoroselenoate linkage is synthesized chemically.

18. A method according to claim 14 wherein the **nucleic acid** is synthesized by copying a **nucleic acid** template using a primer, a polymerase and dNTP-.alpha.-S or dNTP-.alpha.-Se.

25. A method of preparing a **nucleic acid** molecule containing no or up to ten negative charges or a **nucleic acid** molecule containing no or up to ten positive charges wherein the **nucleic acid** molecule has a sugar-linkage-sugar backbone and said sugars have a base attached thereto at the 1 position; said method comprising the steps of (1) synthesizing a **nucleic acid** with a phosphorothioate linkage or a phosphoroselenoate linkage between sugar residues, and (2) reacting the said **nucleic acid** with an alkylating agent so as to eliminate the charge on the said phosphorothioate linkage or said phosphoroselenoate linkage, wherein the **nucleic acid** chain is synthesized enzymatically and is terminated using a ddNTP, a ddNTP-.alpha.-S or a ddNTP-.alpha.-Se.

. . . completely with the phosphorothioate S atom or phosphoroselenoate Se atom and substantially completely with other reactive groups in the said **nucleic acid**.

32. A method of preparing a **nucleic acid** molecule containing one or up to ten negative charges wherein the **nucleic acid** molecule has a sugar-linkage-sugar backbone and said sugars have a base attached thereto at the 1 position; said method comprising the steps of synthesizing enzymatically the said **nucleic acid** using a dNTP uncharged at least at the .alpha.-phosphorus position, wherein the **nucleic acid** is synthesized additionally using a primer and a polymerase and wherein the said dNTP uncharged at least at the .alpha.-phosphorus position is enzymatically incorporated into the said **nucleic acid** molecule.

38. A **nucleic acid** molecule comprising a sugar-linkage-sugar backbone wherein said sugars have a base attached thereto at the 1 position; said molecule further. . .
39. A **nucleic acid** according to claim 38 comprising at least 50 nucleoside residues.

40. A **nucleic acid** with one or up to ten positive charges wherein the sugar-sugar linkages are uncharged.

41. A **nucleic acid** according to claim 40 wherein each sugar-sugar linkage is either an alkylated phosphorothioate moiety or an alkylated phosphoroselenoate moiety.

42. A method of analyzing a **nucleic acid** by mass spectrometry comprising the steps of (1) preparing a **nucleic acid** according to the method of claim 14; (2) introducing the said **nucleic acid** molecule into a mass spectrometer; and (3) determining the mass of the said **nucleic acid**

43. A method according to claim 42 wherein the sugar-sugar linkages of the **nucleic acid** are substantially all phosphate sugar-sugar linkages.

44. A method according to claim 1, wherein said **nucleic acid** molecule comprises a non-phosphate sugar-sugar linkage.

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=> s positiv? (3a) charg? (3a) label? (4a) terminal (4a) (nucleic acid? or oligo? or DNA)
   4 FILES SEARCHED...
L11   1 POSITIV? (3A) CHARG? (3A) LABEL? (4A) TERMINAL (4A) (NUCLEIC
               ACID? OR OLIGO? OR DNA)

=> d l11 bib abs kwic

L11 ANSWER 1 OF 1 USPATFULL
AN   2002:243051 USPATFULL
TI   Compositions and methods for the therapy and diagnosis of ovarian cancer
IN   Algate, Paul A., Issaquah, WA, UNITED STATES
       Jones, Robert, Seattle, WA, UNITED STATES
       Harlocker, Susan L., Seattle, WA, UNITED STATES
PA   Corixa Corporation, Seattle, WA, UNITED STATES, 98104 (U.S. corporation)
PI   US 2002132237   A1   20020919
AI   US 2001-867701   A1   20010529 (9)
PRAI   US 2000-207484P   20000526 (60)
DT   Utility
FS   APPLICATION
LREP   SEED INTELLECTUAL PROPERTY LAW GROUP PLLC, 701 FIFTH AVE, SUITE 6300,
       SEATTLE, WA, 98104-7092
CLMN   Number of Claims: 11
ECL   Exemplary Claim: 1
DRWN   No Drawings
LN.CNT 25718
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB   Compositions and methods for the therapy and diagnosis of cancer,
       particularly ovarian cancer, are disclosed. Illustrative compositions
       comprise one or more ovarian tumor polypeptides, immunogenic portions
       thereof, polynucleotides that encode such polypeptides, antigen
       presenting cell that expresses such polypeptides, and T cells that are
       specific for cells expressing such polypeptides. The disclosed
       compositions are useful, for example, in the diagnosis, prevention
       and/or treatment of diseases, particularly ovarian cancer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.
SUMM   [2043] SEQ ID NO: 2004 represents the cDNA sequence for clone AA165409.

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=> s mass tag
L13         110 MASS TAG

=> s l13 and oligonucleotide?
L14          50 L13 AND OLIGONUCLEOTIDE?

=> s l14 and label?
L15          43 L14 AND LABEL?

=> s l15 and terminal
L16          21 L15 AND TERMINAL

=> dup rem l16
PROCESSING COMPLETED FOR L16
L17          21 DUP REM L16 (0 DUPLICATES REMOVED)

=> d l17 bib abs 1-21

L17  ANSWER 1 OF 21  USPATFULL
AN      2002:322488  USPATFULL
TI      Proteomic analysis
IN      Cravatt, Benjamin F., La Jolla, CA, UNITED STATES
        Sorensen, Erik, San Diego, CA, UNITED STATES
        Patricelli, Matthew P., San Diego, CA, UNITED STATES
        Lovato, Martha, San Diego, CA, UNITED STATES
        Adam, Gregory, San Diego, CA, UNITED STATES
PI      US 2002182652      A1   20021205
AI      US 2002-158498     A1   20020529 (10)
RLI     Division of Ser. No. US 2000-738954, filed on 15 Dec 2000, PENDING
PRAI    US 2000-195954P     20000410 (60)
        US 2000-212891P     20000620 (60)
        US 2000-222532P     20000802 (60)
DT      Utility
FS      APPLICATION
LREP    GARY CARY WARE & FRIENDENRICH LLP, 4365 EXECUTIVE DRIVE, SUITE 1600, SAN
        DIEGO, CA, 92121-2189
CLMN    Number of Claims: 14
ECL     Exemplary Claim: 1
DRWN    24 Drawing Page(s)
LN.CNT 3576
AB      The present invention provides methods for analyzing proteomes, as cells
        or lysates. The analysis is based on the use of probes that have
        specificity to the active form of proteins, particularly enzymes and
        receptors. The probes can be identified in different ways. In accordance
        with the present invention, a method is provided for generating and
        screening compound libraries that are used for the identification of
        lead molecules, and for the parallel identification of their biological
        targets. By appending specific functionalities and/or groups to one or
        more binding moieties, the reactive functionalities gain binding
        affinity and specificity for particular proteins and classes of
        proteins. Such libraries of candidate compounds, referred to herein as
        activity-based probes, or ABPs, are used to screen for one or more
        desired biological activities or target proteins.


L17  ANSWER 2 OF 21  USPATFULL
AN      2002:322437  USPATFULL
TI      Method and reagents for analyzing the nucleotide sequence of nucleic
        acids
IN      Sampson, Jeffrey R., Burlingame, CA, UNITED STATES
        Myerson, Joel, Berkeley, CA, UNITED STATES
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Tsalenko, Anna M., Chicago, IL, UNITED STATES
Sampas, Nicholas M., San Jose, CA, UNITED STATES
Webb, Peter G., Menlo Park, CA, UNITED STATES
Yakhini, Zohar H., Zikhron Ya'Acov, ISRAEL
PI US 2002182601 A1 20021205
AI US 2001-836012 A1 20010417 (9)
RLI Continuation-in-part of Ser. No. US 1998-112437, filed on 9 Jul 1998, GRANTED, Pat. No. US 6218118
DT Utility
FS APPLICATION
LREP AGILENT TECHNOLOGIES, Legal Department, DL429, Intellectual Property Administration, P.O. Box 58043, Santa Clara, CA, 95052-8043
CLMN Number of Claims: 80
ECL Exemplary Claim: 1
DRWN 13 Drawing Page(s)
LN.CNT 3253
AB Methods and reagents are disclosed which provide for more sensitive, more accurate and higher through-put analyses of target nucleic acid sequences. The methods and reagents of the present invention may be generically applied to generally any target nucleic acid sequence and do not require a priori information about the presence, location or identity of mutations in the target nucleic acid sequence. The reagents of the invention are mixtures of **oligonucleotide** precursors having a high level of coverage and mass number complexity, and also having tags analyzable by mass spectrometry which are covalently linked to the precursors through cleavable bonds. A method is also disclosed for analyzing a target nucleic acid sequence employing the mixtures of **oligonucleotide** precursors having tags analyzable by mass spectrometry covalently linked to the **oligonucleotide** precursors through cleavable bonds, and chemical or enzymatic assays to alter the mass of the **oligonucleotide** precursors prior to mass spectral analysis. The enzymatic assay may be a polymerase extension assay or a ligation-based assay. The kits for carrying out the methods of the invention are also disclosed.

L17 ANSWER 3 OF 21 USPATFULL
AN 2002:307838 USPATFULL
TI Mass defect **labeling** for the determination of oligomer sequences
IN Schneider, Luke V., Half Moon Bay, CA, UNITED STATES
Hall, Michael P., San Carlos, CA, UNITED STATES
Petesch, Robert, Newark, CA, UNITED STATES
PA Target Discovery, San Carlos, CA, UNITED STATES, 94070 (U.S. corporation)
PI US 2002172961 A1 20021121
AI US 2001-35349 A1 20011019 (10)
PRAI US 2000-242165P 20001019 (60)
US 2000-242398P 20001019 (60)
DT Utility
FS APPLICATION
LREP TOWNSEND AND TOWNSEND AND CREW, LLP, TWO EMBARCADERO CENTER, EIGHTH FLOOR, SAN FRANCISCO, CA, 94111-3834
CLMN Number of Claims: 50
ECL Exemplary Claim: 1
DRWN 32 Drawing Page(s)
LN.CNT 3568
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Mass tagging methods are provided that lead to mass spectrometer detection sensitivities and molecular discriminations that are improved over other methods. In particular the methods are useful for discriminating tagged molecules and fragments of molecules from chemical

noise in the mass spectrum. These mass tagging methods are useful for oligomer sequencing, determining the relative abundances of molecules from different samples, and identifying individual molecules or chemical processing steps in combinatorial chemical libraries. The methods provided are useful for the simultaneous analysis of multiple molecules and reaction mixtures by mass spectrometric methods.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 4 OF 21 USPATFULL
AN 2002:301101 USPATFULL
TI Methods for isolation and **labeling** of sample molecules
IN Aebersold, Rudolf H., Mercer Island, WA, UNITED STATES
Zhou, Huilin, Seattle, WA, UNITED STATES
PI US 2002168644 A1 20021114
AI US 2001-858198 A1 20010514 (9)
DT Utility
FS APPLICATION
LREP CAMPBELL & FLORES LLP, 4370 LA JOLLA VILLAGE DRIVE, 7TH FLOOR, SAN DIEGO, CA, 92122
CLMN Number of Claims: 105
ECL Exemplary Claim: 1
DRWN 13 Drawing Page(s)
LN.CNT 1592
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides methods for **labeling** a molecule by contacting a sample molecule with a solid support coupled to a chemical group comprising a cleavable functional group, one or more functional groups, and a reactive group for the sample molecule, under conditions allowing the sample molecule to covalently bind to the reactive group; and cleaving the cleavable functional group, thereby releasing the sample molecule comprising the one or more functional groups, which can be a tag. The invention also provides a solid support covalently coupled to a chemical group comprising a cleavable functional group, a mass spectrometry tag and a reactive group for covalently attaching a sample molecule, wherein the cleavable functional group, the tag and the reactive group are positioned relative to each other to allow transfer of the tag to the sample molecule upon cleavage of the cleavable functional group.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 5 OF 21 USPATFULL
AN 2002:258766 USPATFULL
TI Methods for determining a nucleotide at a specific location within a nucleic acid molecule
IN Smith, Douglas R., Gloucester, MA, UNITED STATES
Thomann, Hans-Ulrich, Lexington, MA, UNITED STATES
Cahill, Patrick, Natick, MA, UNITED STATES
PA Genome Therapeutics Corporation, Waltham, MA, UNITED STATES, 02154 (U.S. corporation)
PI US 2002142336 A1 20021003
AI US 2002-61961 A1 20020201 (10)
PRAI US 2001-266035P 20010202 (60)
DT Utility
FS APPLICATION
LREP LAHIVE & COCKFIELD, 28 STATE STREET, BOSTON, MA, 02109
CLMN Number of Claims: 33
ECL Exemplary Claim: 1
DRWN 19 Drawing Page(s)
LN.CNT 2015
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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AB Novel methods for determining the existence or nonexistence of a test nucleotide on a strand of DNA are provided. The methods involve the use of a proofreading polymerase that is capable of incorporating a **labeled** nucleotide in a primer into and extension product if there is a match between the test nucleotide on the strand of DNA and the complementary nucleotide on the primer, but which excises the **labeled** nucleotide and does not incorporate it into an extension product if there is a mismatch. The presence or absence of the test nucleotide then may be established by determining whether the **label** is preserved or lost following the reaction. Methods involving the use of a quencher-chromophore pair are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 6 OF 21 USPATFULL
AN 2002:251742 USPATFULL
TI Base analogues
IN Kumar, Shiv, Belle Mead, NJ, UNITED STATES
Nampalli, Satyam, Belle Mead, NJ, UNITED STATES
Neagu, Constantin, West Windsor, NJ, UNITED STATES
McDougall, Mark, Arroyo Grande, CA, UNITED STATES
Loakes, David, Cambridge, UNITED KINGDOM
Brown, Dan, Cambridge, UNITED KINGDOM
PI US 2002137695 A1 20020926
AI US 2001-898210 A1 20010703 (9)
PRAI GB 2000-16258 20000703
DT Utility
FS APPLICATION
LREP Amersham Pharmacia Biotech, Inc., 800 Centennial Avenue, Piscataway, NJ, 08855
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 619
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention describes novel compounds of the formula formula ##STR1##

Wherein Q is H or a sugar or a sugar analogue or a nucleic acid backbone or backbone analogue, Y=0 O, S, NR.sup.10, where R.sup.10 is H, alkyl alkenyl, alkynyl, X is H, alkyl, alkenyl, alkynyl, aryl, heteroaryl or a combination thereof or, preferably, a reporter group. The novel compounds are suitable for incorporation in **oligonucleotides** and polynucleotides.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 7 OF 21 USPATFULL
AN 2002:251113 USPATFULL
TI Rapid, quantitative method for the mass spectrometric analysis of nucleic acids for gene expression and genotyping
IN Wold, Barbara J., Pasadena, CA, UNITED STATES
Murphy, John F., Pasadena, CA, UNITED STATES
Davis, Mark E., Pasadena, CA, UNITED STATES
Kirshenbaum, Kent, Pasadena, CA, UNITED STATES
Tirrell, David A., Pasadena, CA, UNITED STATES
PI US 2002137057 A1 20020926
AI US 2001-918687 A1 20010727 (9)
PRAI US 2000-221479P 20000727 (60)
DT Utility
FS APPLICATION
LREP Lisa A. Haile, J.D., Ph.D., GRAY CARY WARE & FREIDENRICH LLP, 4365

Executive Drive, Suite 1600, San Diego, CA, 92121-2189
CLMN Number of Claims: 38
ECL Exemplary Claim: 1
DRWN 25 Drawing Page(s)
LN.CNT 1674
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention provides methods of identifying one or more nucleic acids in a sample. The nucleic acids, for example, expressed genes in a cell, can be identified by contacting the nucleic acids with **oligonucleotides** having detector tags, and selector tags to form tagged **oligonucleotides**. Each nucleic acid can be uniquely identified by mass-spectrophotometric analysis of the detector tag.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 8 OF 21 USPATFULL
AN 2002:198549 USPATFULL
TI Fixed address analysis of sequence tags
IN Lizardi, Paul M., Wallingford, CT, UNITED STATES
Roth, Matthew E., Branford, CT, UNITED STATES
Feng, Li, Hamden, CT, UNITED STATES
Guerra, Cesar E., Guilford, CT, UNITED STATES
Weber, Shane C., Woodbridge, CT, UNITED STATES
Kaufman, Joseph C., Hamden, CT, UNITED STATES
Latimer, Darin R., East Haven, CT, UNITED STATES
PA Yale University (U.S. corporation)
PI US 2002106649 A1 20020808
AI US 2001-855793 A1 20010515 (9)
RLI Continuation of Ser. No. US 2000-544713, filed on 6 Apr 2000, PATENTED
PRAI US 1999-127932P 19990406 (60)
DT Utility
FS APPLICATION
LREP Robert A. Hodges, NEEDLE & ROSENBERG, P.C., The Candler Building, Suite 1200, 127 Peachtree Street, N.E., Atlanta, GA, 30303-1811
CLMN Number of Claims: 154
ECL Exemplary Claim: 1
DRWN 5 Drawing Page(s)
LN.CNT 4340
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is a method for the comprehensive analysis of nucleic acid samples and a detector composition for use in the method. The method, referred to as Fixed Address Analysis of Sequence Tags (FAAST), involves generation of a set of nucleic acid fragments having a variety of sticky end sequences; indexing of the fragments into sets based on the sequence of sticky ends; associating a detector sequence with the fragments; sequence-based capture of the indexed fragments on a detector array; and detection of the fragment **labels**. Generation of the multiple sticky end sequences is accomplished by incubating the nucleic acid sample with one or more nucleic acid cleaving reagents. The indexed fragments are captured by hybridization and coupling, preferably by ligation, to a probe. The method allows a complex sample of nucleic acid to be quickly and easily cataloged in a reproducible and sequence-specific manner. One form of the method allows determination of associations, in a nucleic acid molecule, of different combinations of known or potential sequences. Another form of the method assesses modification of sequences in nucleic acid molecules by basing cleavage of the molecules on the presence or absence of modification.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 9 OF 21 USPATFULL
AN 2002:127090 USPATFULL

09567863

TI Methods for the survey and genetic analysis of populations
IN Ashby, Matthew, Mill Valley, CA, UNITED STATES
PI US 2002065609 A1 20020530
AI US 2001-829855 A1 20010410 (9)
PRAI US 2000-196063P 20000410 (60)
US 2000-196258P 20000411 (60)
DT Utility
FS APPLICATION
LREP James F. Haley, Jr., FISH & NEAVE, 1251 Avenue of the Americas, New York, NY, 10020-1104
CLMN Number of Claims: 44
ECL Exemplary Claim: 1
DRWN 18 Drawing Page(s)
LN.CNT 2019
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to methods for performing surveys of the genetic diversity of a population. The invention also relates to methods for performing genetic analyses of a population. The invention further relates to methods for the creation of databases comprising the survey information and the databases created by these methods. The invention also relates to methods for analyzing the information to correlate the presence of nucleic acid markers with desired parameters in a sample. These methods have application in the fields of geochemical exploration, agriculture, bioremediation, environmental analysis, clinical microbiology, forensic science and medicine.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 10 OF 21 USPATFULL
AN 2002:126287 USPATFULL
TI Proteomic analysis
IN Cravatt, Benjamin F., La Jolla, CA, UNITED STATES
Sorensen, Erik, San Diego, CA, UNITED STATES
Patricelli, Matthew P., San Diego, CA, UNITED STATES
Lovato, Martha, San Diego, CA, UNITED STATES
Adam, Gregory, San Diego, CA, UNITED STATES
PA The Scripps Research Institute of an Assignment (U.S. corporation)
PI US 2002064799 A1 20020530
AI US 2001-836145 A1 20010416 (9)
RLI Continuation of Ser. No. US 2000-738271, filed on 15 Dec 2000, PENDING
PRAI US 2000-195954P 20000410 (60)
US 2000-212891P 20000620 (60)
US 2000-222532P 20000802 (60)
DT Utility
FS APPLICATION
LREP Lisa A. Haile, Ph.D., Gray Cary Ware & Freidenrich LLP, Suite 1600, 4365 Executive Drive, San Diego, CA, 92121-2189
CLMN Number of Claims: 13
ECL Exemplary Claim: 1
DRWN 24 Drawing Page(s)
LN.CNT 3602
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides methods for analyzing proteomes, as cells or lysates. The analysis is based on the use of probes that have specificity to the active form of proteins, particularly enzymes and receptors. The probes can be identified in different ways. In accordance with the present invention, a method is provided for generating and screening compound libraries that are used for the identification of lead molecules, and for the parallel identification of their biological targets. By appending specific functionalities and/or groups to one or more binding moieties, the reactive functionalities gain binding affinity and specificity for particular proteins and classes of

proteins. Such libraries of candidate compounds, referred to herein as activity-based probes, or ABPs, are used to screen for one or more desired biological activities or target proteins.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 11 OF 21 USPATFULL
AN 2002:85154 USPATFULL
TI Proteomic analysis
IN Cravatt, Benjamin F., La Jolla, CA, UNITED STATES
Sorensen, Erik, San Diego, CA, UNITED STATES
Patricelli, Matthew P., San Diego, CA, UNITED STATES
Lovato, Martha, San Diego, CA, UNITED STATES
Adam, Gregory, San Diego, CA, UNITED STATES
PI US 2002045194 A1 20020418
AI US 2000-738954 A1 20001215 (9)
PRAI US 2000-195954P 20000410 (60)
US 2000-212891P 20000620 (60)
US 2000-222532P 20000802 (60)
DT Utility
FS APPLICATION
LREP Lisa A. Haile, Ph.D., Gray Cary Ware & Freidenrich LLP, Suite 1600, 4365 Executive Drive, San Diego, CA, 92121-2189
CLMN Number of Claims: 31
ECL Exemplary Claim: 1
DRWN 24 Drawing Page(s)
LN.CNT 3728
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides methods for analyzing proteomes, as cells or lysates. The analysis is based on the use of probes that have specificity to the active form of proteins, particularly enzymes and receptors. The probes can be identified in different ways. In accordance with the present invention, a method is provided for generating and screening compound libraries that are used for the identification of lead molecules, and for the parallel identification of their biological targets. By appending specific functionalities and/or groups to one or more binding moieties, the reactive functionalities gain binding affinity and specificity for particular proteins and classes of proteins. Such libraries of candidate compounds, referred to herein as activity-based probes, or ABPs, are used to screen for one or more desired biological activities or target proteins.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 12 OF 21 USPATFULL
AN 2002:73134 USPATFULL
TI Proteomic analysis
IN Cravatt, Benjamin F., La Jolla, CA, UNITED STATES
Sorensen, Erik, San Diego, CA, UNITED STATES
Patricelli, Matthew P., San Diego, CA, UNITED STATES
Lovato, Martha, San Diego, CA, UNITED STATES
Adam, Gregory, San Diego, CA, UNITED STATES
PA The Scripps Research Institute (U.S. corporation)
PI US 2002040275 A1 20020404
AI US 2001-836148 A1 20010416 (9)
RLI Continuation of Ser. No. US 2000-738954, filed on 15 Dec 2000, PENDING
PRAI US 2000-195954P 20000410 (60)
US 2000-212891P 20000620 (60)
US 2000-222532P 20000802 (60)
DT Utility
FS APPLICATION
LREP Lisa A. Haile, Ph.D., Gray Cary Ware & Freidenrich LLP, Suite 1600, 4365

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Executive Drive, San Diego, CA, 92121-2189
CLMN Number of Claims: 15
ECL Exemplary Claim: 1
DRWN 24 Drawing Page(s)
LN.CNT 3667
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides methods for analyzing proteomes, as cells or lysates. The analysis is based on the use of probes that have specificity to the active form of proteins, particularly enzymes and receptors. The probes can be identified in different ways. In accordance with the present invention, a method is provided for generating and screening compound libraries that are used for the identification of lead molecules, and for the parallel identification of their biological targets. By appending specific functionalities and/or groups to one or more binding moieties, the reactive functionalities gain binding affinity and specificity for particular proteins and classes of proteins. Such libraries of candidate compounds, referred to herein as activity-based probes, or ABPs, are used to screen for one or more desired biological activities or target proteins.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 13 OF 21 USPATFULL
AN 2002:43173 USPATFULL
TI Methods for preparing conjugates
IN Dellinger, Douglas J., Sunnyvale, CA, UNITED STATES
Myerson, Joel, Berkeley, CA, UNITED STATES
Fulcrand, Geraldine, Sunnyvale, CA, UNITED STATES
Ilsley, Diane D., San Jose, CA, UNITED STATES
PI US 2002025539 A1 20020228
AI US 2001-981580 A1 20011017 (9)
RLI Division of Ser. No. US 1999-397526, filed on 16 Sep 1999, PENDING
DT Utility
FS APPLICATION
LREP AGILENT TECHNOLOGIES, INC., Legal Department, DL429, Intellectual Property Administration, P. O. Box 7599, Loveland, CO, 80537-0599
CLMN Number of Claims: 45
ECL Exemplary Claim: 1
DRWN 2 Drawing Page(s)
LN.CNT 1750
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods are disclosed for conjugating one moiety to another moiety. In the method the moieties are reacted with one another in a protic solvent. Reaction between the moieties and the protic solvent during the conjugating is negligible or reversible. A stable bond is formed between the moieties to produce a product that is not subject to .beta.-elimination at elevated pH. Usually, one of the moieties comprises an unsaturation between two carbon atoms. One of the carbon atoms is or becomes an electrophile during the conjugating. The other of the moieties comprises a functionality reactive with the electrophile carbon atom to form a product that comprises the unsaturation. Compounds comprising both of the moieties as well as precursor molecules are also disclosed. Methods are also disclosed for determining an analyte in a sample employing compounds as described above.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 14 OF 21 USPATFULL
AN 2002:298463 USPATFULL
TI Parallel methods for genomic analysis
IN Strathmann, Michael P., 1674 Euclid Ave., Berkeley, CA, United States 94709

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PI US 6480791 B1 20021112
AI US 1999-427834 19991026 (9)
PRAI US 1998-105914P 19981028 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Brusca, John S.; Assistant Examiner: Moran, Marjorie A.
LREP McCutchen, Doyle, Brown & Enersen, LLP, Shuster, Michael J.
CLMN Number of Claims: 30
ECL Exemplary Claim: 1
DRWN 10 Drawing Figure(s); 8 Drawing Page(s)
LN.CNT 4843
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention provides parallel methods for determining nucleotide sequences and physical maps of polynucleotides associated with sample tags. This information can be used to determine the chromosomal locations of sample-tagged polynucleotides. In one embodiment, the polynucleotides are derived from genomic DNA coupled to insertion elements. As a result, the invention also provides parallel methods for locating the integration sites of insertion elements in the genome.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 15 OF 21 USPATFULL
AN 2002:262204 USPATFULL
TI Methods for controlling cross-hybridization in analysis of nucleic acid sequences
IN Wolber, Paul K., Los Altos, CA, United States
Kincaid, Robert H., Half Moon Bay, CA, United States
PA Agilent Technologies, Inc., Palo Alto, CA, United States (U.S. corporation)
PI US 6461816 B1 20021008
AI US 1999-350969 19990709 (9)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Brusca, John S.; Assistant Examiner: Kim, Young
CLMN Number of Claims: 28
ECL Exemplary Claim: 1
DRWN 0 Drawing Figure(s); 0 Drawing Page(s)
LN.CNT 2702
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods, reagents and kits are disclosed for selecting target-specific **oligonucleotide** probes, which may be used in analyzing a target nucleic acid sequence. In one aspect the present invention is directed to selecting a set of target-specific **oligonucleotide** probes. A cross-hybridization **oligonucleotide** probe is identified based on a candidate target-specific **oligonucleotide** probe for the target nucleic acid sequence. The cross-hybridization **oligonucleotide** probe measures the extent of occurrence of a cross-hybridization event having a predetermined probability. Cross-hybridization results are determined employing the cross-hybridization **oligonucleotide** probe and the target-specific **oligonucleotide** probe. The target-specific **oligonucleotide** probe is selected or rejected for the set based on the cross-hybridization results.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 16 OF 21 USPATFULL
AN 2002:224621 USPATFULL
TI Base analogues

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IN Simmonds, Adrian Christopher, Amersham, UNITED KINGDOM
Hamilton, Alan, Amersham, UNITED KINGDOM
Smith, Clifford, Tring, UNITED KINGDOM
Loakes, David, Letchworth, UNITED KINGDOM
Brown, Daniel, Cambridge, UNITED KINGDOM
Hill, Fergal, Cambridge, UNITED KINGDOM
Kumar, Shiv, Belle Mead, NJ, United States
Nampalli, Satyam, Belle Mead, NJ, United States
McDougall, Mark, Bethlehem, PA, United States
PA Nycomed Amersham PLC, Buckinghamshire, UNITED KINGDOM (non-U.S. corporation)
PI US 6444682 B1 20020903
AI US 2000-463501 20000418 (9)
PRAI GB 1997-16231 19970731
DT Utility
FS GRANTED
EXNAM Primary Examiner: Shah, Mukund J.; Assistant Examiner: Patel, Sudhaker B.
LREP Marshall, Gerstein & Borun
CLMN Number of Claims: 14
ECL Exemplary Claim: 1
DRWN 0 Drawing Figure(s); 0 Drawing Page(s)
LN.CNT 1300
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Nucleotide or base analogues having structure (3) or (4) ##STR1##

wherein X.dbd.O or NH or S and

each R.sup.6 is independently H or alkyl or alkenyl or alkoxy or aryl or a reporter moiety.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 17 OF 21 USPATFULL
AN 2002:136767 USPATFULL
TI Analysis of sequence tags with hairpin primers
IN Lizardi, Paul M., Wallingford, CT, United States
Latimer, Darin R., East Haven, CT, United States
PA Yale University, New Haven, CT, United States (U.S. corporation)
PI US 6403319 B1 20020611
AI US 2000-637384 20000811 (9)
RLI Continuation-in-part of Ser. No. US 2000-544713, filed on 6 Apr 2000, now patented, Pat. No. US 6261782
PRAI US 1999-148870P 19990813 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Needle & Rosenberg, P.C.
CLMN Number of Claims: 106
ECL Exemplary Claim: 1
DRWN 7 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 3134
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is a method for the comprehensive analysis of nucleic acid samples and a detector composition for use in the method. The method involves amplifying nucleic acid fragments of interest using a primer that can form a hairpin structure; sequence-based coupling of the amplified fragments to detector probes; and detection of the coupled fragments. The amplified fragments are coupled by hybridization and coupling, preferably by ligation, to detector probes. A hairpin structure formed at the end of the amplified fragments facilitates coupling of the fragments to the probes. The method allows detection of

the fragments where detection provides some sequence information for the fragments. The method allows a complex sample of nucleic acid to be quickly and easily cataloged in a reproducible and sequence-specific manner. The method can also be used to detect amplified fragments having a known sequence.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 18 OF 21 USPATFULL
AN 2002:102268 USPATFULL
TI Binary encoded sequence tags
IN Kaufman, Joseph C., Hamden, CT, United States
Roth, Matthew E., Branford, CT, United States
Lizardi, Paul M., Wallingford, CT, United States
Feng, Li, Hamden, CT, United States
Latimer, Darin R., East Haven, CT, United States
PA Yale University, United States (U.S. corporation)
Agilix Corporation, United States (U.S. corporation)
PI US 6383754 B1 20020507
AI US 2000-637751 20000811 (9)
RLI Continuation-in-part of Ser. No. US 2000-544713, filed on 6 Apr 2000, now patented, Pat. No. US 6261782
PRAI US 1999-148870P 19990813 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Needle & Rosenberg, P.C.
CLMN Number of Claims: 131
ECL Exemplary Claim: 1
DRWN 3 Drawing Figure(s); 3 Drawing Page(s)
LN.CNT 3871
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is a method for the comprehensive analysis of nucleic acid samples and a detector composition for use in the method. The method, referred to as Binary Encoded Sequence Tags (BEST), involves generation of a set of nucleic acid fragments; adding an adaptor to the ends containing recognition site for cleavage at a site offset from the recognition site; cleaving the fragment to generate fragments having a plurality sticky ends; indexing of the fragments into sets based on the sequence of sticky ends. The fragments are indexed by adding a offset adaptor to newly generated ends. A different adaptor will be coupled to each different sticky end. The resulting fragments--which will have defined ends, be of equal lengths (in preferred embodiment), and a central sequence derived from the source nucleic acid molecule--are binary sequence tags. The binary sequence tags can be used and further analyzed in numerous ways. For example, the binary sequence tags can be captured by hybridization and coupling, preferably by ligation, to a probe. The probe is preferably immobilized in an array or on sortable beads. One form of the BEST method, referred to as modification assisted analysis of binary sequence tags (MAABST), assesses modification of sequences in nucleic acid molecules by detecting differential cleavage based on the presence or absence of modification in the molecules.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 19 OF 21 USPATFULL
AN 2001:112050 USPATFULL
TI Fixed address analysis of sequence tags
IN Lizardi, Paul M., Wallingford, CT, United States
Roth, Matthew E., Branford, CT, United States
Feng, Li, Hamden, CT, United States
Guerra, Cesar E., Guilford, CT, United States

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Weber, Shane C., Woodbridge, CT, United States
Kaufman, Joseph C., Hamden, CT, United States
Latimer, Darin R., East Haven, CT, United States
PA Yale University, New Haven, CT, United States (U.S. corporation)
PI US 6261782 B1 20010717
AI US 2000-544713 20000406 (9)
PRAI US 1999-127932P 19990406 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Horlick, Kenneth R.
LREP Needle & Rosenberg, P.C.
CLMN Number of Claims: 154
ECL Exemplary Claim: 1
DRWN 5 Drawing Figure(s); 5 Drawing Page(s)
LN.CNT 4505
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Disclosed is a method for the comprehensive analysis of nucleic acid samples and a detector composition for use in the method. The method, referred to as Fixed Address Analysis of Sequence Tags (FAAST), involves generation of a set of nucleic acid fragments having a variety of sticky end sequences; indexing of the fragments into sets based on the sequence of sticky ends; associating a detector sequence with the fragments; sequence-based capture of the indexed fragments on a detector array; and detection of the fragment **labels**. Generation of the multiple sticky end sequences is accomplished by incubating the nucleic acid sample with one or more nucleic acid cleaving reagents. The indexed fragments are captured by hybridization and coupling, preferably by ligation, to a probe. The method allows a complex sample of nucleic acid to be quickly and easily cataloged in a reproducible and sequence-specific manner. One form of the method allows determination of associations, in a nucleic acid molecule, of different combinations of known or potential sequences. Another form of the method assesses modification of sequences in nucleic acid molecules by basing cleavage of the molecules on the presence or absence of modification.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 20 OF 21 USPATFULL
AN 2001:56106 USPATFULL
TI Compounds and methods for detecting biomolecules
IN Rothschild, Kenneth J., Newton, MA, United States
Olejnik, Jerzy, Brookline, MA, United States
PA AmberGen Inc., Boston, MA, United States (U.S. corporation)
PI US 6218530 B1 20010417
AI US 1999-323424 19990601 (9)
PRAI US 1998-87641P 19980602 (60)
DT Utility
FS Granted
EXNAM Primary Examiner: Riley, Jezia
LREP Medlen & Carroll, LLP
CLMN Number of Claims: 12
ECL Exemplary Claim: 1
DRWN 10 Drawing Figure(s); 9 Drawing Page(s)
LN.CNT 728
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods are described for synthesizing compounds useful for detecting nucleic acids, and in particular, the hybridization of nucleic acids. Photocleavable agents are described, including but not limited to photocleavable nucleotides and photocleavable phosphoramidites.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

09567863

L17 ANSWER 21 OF 21 USPATFULL
AN 2001:55695 USPATFULL
TI Method and mixture reagents for analyzing the nucleotide sequence of nucleic acids by mass spectrometry
IN Sampson, Jeffrey R., Burlingame, CA, United States
Yakhini, Zohar H., Palo Alto, CA, United States
Webb, Peter G., Menlo Park, CA, United States
Sampas, Nicholas M., San Jose, CA, United States
Tsalenko, Anna M., Chicago, IL, United States
Myerson, Joel, Berkeley, CA, United States
PA Agilent Technologies, Inc., Palo Alto, CA, United States (U.S. corporation)
PI US 6218118 B1 20010417
AI US 1998-112437 19980709 (9)
DT Utility
FS Granted
EXNAM Primary Examiner: Horlick, Kenneth R.; Assistant Examiner: Siew, Jeffrey
CLMN Number of Claims: 70
ECL Exemplary Claim: 1
DRWN 26 Drawing Figure(s); 22 Drawing Page(s)
LN.CNT 2982
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods and reagents are disclosed which satisfy the need for more sensitive, more accurate and higher through-put analyses of target nucleic acid sequences. The methods and reagents may be generically applied to generally any target nucleic acid sequence and do not require a priori information about the presence, location or identity of mutations in the target nucleic acid sequence. The reagents of the invention are mixtures of natural and mass-modified **oligonucleotide** precursors having a high level of coverage and mass number complexity. A method is also disclosed for analyzing a target nucleic acid sequence employing the mixtures of natural and mass-modified **oligonucleotide** precursors and chemical or enzymatic assays to alter the mass of the **oligonucleotide** precursors prior to mass spectral analysis, generally via MALDI-TOF. The enzymatic assay may be a polymerase extension assay or a ligase assay. The kits for carrying out the methods of the invention are also disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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     (FILE 'HOME' ENTERED AT 10:12:59 ON 18 DEC 2002)

     FILE 'BIOSIS, MEDLINE, CAPLUS, WPIDS, USPATFULL' ENTERED AT 10:13:34 ON
     18 DEC 2002
L1       343861 S NUCLEIC ACID
L2            2 S L1 AND POSITIV? (3A) CHARGE TAG (3A) NUCLEIC ACID?
L3           21 S L1 AND POSITIV? (4A) CHARG? (3A) TAG?
L4           19 S L3 NOT L2
L5           19 DUP REM L4 (0 DUPLICATES REMOVED)
L6          109 S L1 AND POSITIV? (4A) LABEL
L7          108 S L6 NOT L5
L8           92 S L7 AND PHOSPHAT?
L9           92 DUP REM L8 (0 DUPLICATES REMOVED)
L10          22 S L9 AND POSITIV? (4A) CHARG?
L11           1 S POSITIV? (3A) CHARG? (3A) LABEL? (4A) TERMINAL (4A) (NUCLEIC
L12           1 S L11 AND POSITIV?
L13         110 S MASS TAG
L14          50 S L13 AND OLIGONUCLEOTIDE?
L15          43 S L14 AND LABEL?
L16          21 S L15 AND TERMINAL
L17          21 DUP REM L16 (0 DUPLICATES REMOVED)

=> s positiv? charg? label? oligonucleotide?
L18           1 POSITIV? CHARG? LABEL? OLIGONUCLEOTIDE?

=> d l18 bib abs

L18  ANSWER 1 OF 1  USPATFULL
AN     2002:236261  USPATFULL
TI     Charge tags and the separation of nucleic acid molecules
IN     Lyamichev, Victor, Madison, WI, UNITED STATES
       Skrzpczynski, Zbigniew, Verona, WI, UNITED STATES
       Allawi, Hatim T., Madison, WI, UNITED STATES
       Wayland, Sarah R., Madison, WI, UNITED STATES
       Takova, Tsetska, Madison, WI, UNITED STATES
       Neri, Bruce P., Madison, WI, UNITED STATES
PA     Third Wave Technologies, Inc. (U.S. corporation)
PI     US 2002128465      A1   20020912
AI     US 2001-777430     A1   20010206 (9)
RLI    Continuation-in-part of Ser. No. US 1999-333145, filed on 14 Jun 1999,
       PENDING Continuation-in-part of Ser. No. US 1996-682853, filed on 12 Jul
       1996, GRANTED, Pat. No. US 6001567
DT     Utility
FS     APPLICATION
LREP   MEDLEN & CARROLL, LLP, 101 HOWARD STREET, SUITE 350, SAN FRANCISCO, CA,
       94105
CLMN   Number of Claims: 86
ECL    Exemplary Claim: 1
DRWN   46 Drawing Page(s)
LN.CNT 5163
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB     The present invention relates to novel phosphoramidites, including
       positive and neutrally charged compounds. The present invention also
       provides charge tags for attachment to materials including solid
       supports and nucleic acids, wherein the charge tags increase or decrease
       the net charge of the material. The present invention further provides
       methods for separating and characterizing molecules based on the charge
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differentials between modified and unmodified materials.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=>

=> d l23 1-2 bib abs

L23 ANSWER 1 OF 2 WPIDS (C) 2002 THOMSON DERWENT
AN 2002-674850 [72] WPIDS
CR 1997-393613 [36]
DNC C2002-190055
TI Composition useful for e.g. separation of nucleic acids comprises a positively or neutrally charged **phosphoramidite**.
DC B04 B05 D16
IN ALLAWI, H T; LYAMICHEV, V; NERI, B P; SKRZPCZYNSKI, Z; TAKOVA, T; WAYLAND, S R
PA (THIR-N) THIRD WAVE TECHNOLOGIES INC
CYC 100
PI WO 2002063030 A2 20020815 (200272)* EN 197p
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW
US 2002128465 A1 20020912 (200272)
ADT WO 2002063030 A2 WO 2002-US3423 20020206; US 2002128465 A1 CIP of US 1996-682853 19960712, CIP of US 1999-333145 19990614, US 2001-777430 20010206
FDT US 2002128465 A1 CIP of US 6001567
PRAI US 2001-777430 20010206; US 1996-682853 19960712; US 1999-333145 19990614
AN 2002-674850 [72] WPIDS
CR 1997-393613 [36]
AB WO 200263030 A UPAB: 20021108
NOVELTY - Composition comprises a positively or neutrally charged **phosphoramidite**.

DETAILED DESCRIPTION - Composition (c) or (c') comprises a positively charged **phosphoramidite** of formula (I) or a neutrally charged **phosphoramidite** of formula (II). (I) comprises nitrogen-containing chemical group selected from primary, secondary or tertiary **amine** or **ammonium** group. (II) comprises secondary or tertiary **amine** or **ammonium** group.

X, Z = a reactive phosphate group;
Y = a protected hydroxy group;
X' = a protected hydroxy group;
N, N' = an **amine** group.

INDEPENDENT CLAIMS are included for the following:

(1) a composition (c1) comprising a charge tag (x1) attached to a terminal end of a nucleic acid molecule, the charge tag comprises a phosphate group and a positively charged molecule;

(2) a composition (c2) comprising a nucleic acid molecule that comprises a positively charged **phosphoramidite**;

(3) a composition (c3) comprising a charge tag attached to the terminal end of a nucleic acid molecule, the charge tag comprises a positively charged **phosphoramidite**;

(4) a composition (c4) comprising a fluorescent dye directly bonded to a phosphate group, which is not directly bonded to an **amine** group;

(5) a mixture (m) comprising a number of oligonucleotides, each oligonucleotide is attached to a different charge tag with each charge tag comprising a phosphate group and a positively charged group;

(6) a composition (c5) comprising a solid support attached to a charged tag, the charge tag comprises a positively charged group and a reactive group configured to allow the charge tag to covalently attach to

the nucleic acid molecule;

(7) separating nucleic acid molecules involving either:

(a) treating (m1) a charge-balanced oligonucleotide containing the charge tag to produce a charge-unbalanced oligonucleotide and separating the charge-unbalanced oligonucleotide from the reaction mixture; or

(b) treating (m2) a number of charge-balanced oligonucleotides, each containing different charge tags, to produce at least 2 charge-unbalanced oligonucleotides, and separating the charge-unbalanced oligonucleotides from the reaction mixture.

USE - The composition is useful for separation of nucleic acid molecules (claimed). The composition is further useful for fractionation of specific nucleic acids by selective charge reversal useful in e.g. INVADER assay cleavage reactions; and in the synthesis of charge-balanced molecules.

ADVANTAGE - In the fractionation of nucleic acid molecules, the method provides an absolute readout of the partition of products from substrates (i.e. provides a 100% separation). Through the use of multiple positively charged adducts, synthetic molecules can be constructed with sufficient modification due to the fact that the normally negatively charged strand is made nearly neutral. It is also possible to distinguish between a enzymatically or thermally degraded DNA fragments due to the absence or presence of 3'phosphate.

Dwg.0/46

L23 ANSWER 2 OF 2 USPATFULL
AN 2002:236261 USPATFULL
TI Charge tags and the separation of nucleic acid molecules
IN Lyamichev, Victor, Madison, WI, UNITED STATES
Skrzpczynski, Zbigniew, Verona, WI, UNITED STATES
Allawi, Hatim T., Madison, WI, UNITED STATES
Wayland, Sarah R., Madison, WI, UNITED STATES
Takova, Tsetska, Madison, WI, UNITED STATES
Neri, Bruce P., Madison, WI, UNITED STATES
PA Third Wave Technologies, Inc. (U.S. corporation)
PI US 2002128465 A1 20020912
AI US 2001-777430 A1 20010206 (9)
RLI Continuation-in-part of Ser. No. US 1999-333145, filed on 14 Jun 1999, PENDING Continuation-in-part of Ser. No. US 1996-682853, filed on 12 Jul 1996, GRANTED, Pat. No. US 6001567
DT Utility
FS APPLICATION
LREP MEDLEN & CARROLL, LLP, 101 HOWARD STREET, SUITE 350, SAN FRANCISCO, CA, 94105
CLMN Number of Claims: 86
ECL Exemplary Claim: 1
DRWN 46 Drawing Page(s)
LN.CNT 5163
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to novel phosphoramidites, including positive and neutrally charged compounds. The present invention also provides charge tags for attachment to materials including solid supports and nucleic acids, wherein the charge tags increase or decrease the net charge of the material. The present invention further provides methods for separating and characterizing molecules based on the charge differentials between modified and unmodified materials.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> s l22 not l23
L24 21 L22 NOT L23

09567863

=> d l24 bib abs 1-21

L24 ANSWER 1 OF 21 USPATFULL
AN 2002:290760 USPATFULL
TI PARG, a GTPase activating protein which interacts with PTPL1
IN Saras, Jan, Uppsala, SWEDEN
Franzen, Petra, Uppsala, SWEDEN
Aspenstrom, Pontus, Uppsala, SWEDEN
Hellman, Ulf, Uppsala, SWEDEN
Gonez, Leonel Jorge, Victoria, AUSTRALIA
Heldin, Carl-Henrik, Uppsala, SWEDEN
PA Ludwig Institute for Cancer Research, New York, NY, United States (U.S. corporation)
PI US 6475775 B1 20021105
AI US 2000-566076 20000508 (9)
RLI Division of Ser. No. US 1998-80855, filed on 18 May 1998, now patented, Pat. No. US 6083721 Continuation of Ser. No. US 1997-805583, filed on 25 Feb 1997, now abandoned
DT Utility
FS GRANTED
EXNAM Primary Examiner: McKelvey, Terry
LREP Wolf, Greenfield & Sacks, P.C.
CLMN Number of Claims: 11
ECL Exemplary Claim: 1
DRWN 12 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 2870
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention describes nucleic acids encoding the PARG protein, including fragments and biologically functional variants thereof. Also included are polypeptides and fragments thereof encoded by such nucleic acids, and antibodies relating thereto. Methods and products for using such nucleic acids and polypeptides also are provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 2 OF 21 USPATFULL
AN 2002:272761 USPATFULL
TI Directed evolution of novel binding proteins
IN Ladner, Robert Charles, Ijamsville, MD, UNITED STATES
Guterman, Sonia Kosow, Belmont, MA, UNITED STATES
Roberts, Bruce Lindsay, Milford, MA, UNITED STATES
Markland, William, Milford, MA, UNITED STATES
Ley, Arthur Charles, Newton, MA, UNITED STATES
Kent, Rachel Baribault, Boxborough, MA, UNITED STATES
PI US 2002150881 A1 20021017
AI US 2001-781988 A1 20010214 (9)
RLI Continuation of Ser. No. US 1998-192067, filed on 16 Nov 1998, ABANDONED Continuation of Ser. No. US 1995-415922, filed on 3 Apr 1995, PATENTED Continuation of Ser. No. US 1993-9319, filed on 26 Jan 1993, PATENTED Division of Ser. No. US 1991-664989, filed on 1 Mar 1991, PATENTED Continuation-in-part of Ser. No. US 1990-487063, filed on 2 Mar 1990, ABANDONED Continuation-in-part of Ser. No. US 1988-240160, filed on 2 Sep 1988, ABANDONED
PRAI WO 1989-US3731 19890901
DT Utility
FS APPLICATION
LREP BROWDY AND NEIMARK, P.L.L.C., 624 Ninth Street, N.W., Washington, DC, 20001
CLMN Number of Claims: 18
ECL Exemplary Claim: 1
DRWN 16 Drawing Page(s)
LN.CNT 15696

09567863

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB In order to obtain a novel binding protein against a chosen target, DNA molecules, each encoding a protein comprising one of a family of similar potential binding domains and a structural signal calling for the display of the protein on the outer surface of a chosen bacterial cell, bacterial spore or phage (genetic package) are introduced into a genetic package. The protein is expressed and the potential binding domain is displayed on the outer surface of the package. The cells or viruses bearing the binding domains which recognize the target molecule are isolated and amplified. The successful binding domains are then characterized. One or more of these successful binding domains is used as a model for the design of a new family of potential binding domains, and the process is repeated until a novel binding domain having a desired affinity for the target molecule is obtained. In one embodiment, the first family of potential binding domains is related to bovine pancreatic trypsin inhibitor, the genetic package is M13 phage, and the protein includes the outer surface transport signal of the M13 gene III protein.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 3 OF 21 USPATFULL
AN 2002:243051 USPATFULL
TI Compositions and methods for the therapy and diagnosis of ovarian cancer
IN Algate, Paul A., Issaquah, WA, UNITED STATES
Jones, Robert, Seattle, WA, UNITED STATES
Harlocker, Susan L., Seattle, WA, UNITED STATES
PA Corixa Corporation, Seattle, WA, UNITED STATES, 98104 (U.S. corporation)
PI US 2002132237 A1 20020919
AI US 2001-867701 A1 20010529 (9)
PRAI US 2000-207484P 20000526 (60)
DT Utility
FS APPLICATION
LREP SEED INTELLECTUAL PROPERTY LAW GROUP PLLC, 701 FIFTH AVE, SUITE 6300, SEATTLE, WA, 98104-7092
CLMN Number of Claims: 11
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 25718
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Compositions and methods for the therapy and diagnosis of cancer, particularly ovarian cancer, are disclosed. Illustrative compositions comprise one or more ovarian tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly ovarian cancer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 4 OF 21 USPATFULL
AN 2002:242791 USPATFULL
TI Compositions and methods for the therapy and diagnosis of colon cancer
IN King, Gordon E., Shoreline, WA, UNITED STATES
Meagher, Madeleine Joy, Seattle, WA, UNITED STATES
Xu, Jiangchun, Bellevue, WA, UNITED STATES
Secrist, Heather, Seattle, WA, UNITED STATES
PA Corixa Corporation, Seattle, WA, UNITED STATES (U.S. corporation)
PI US 2002131971 A1 20020919
AI US 2001-33528 A1 20011226 (10)
RLI Continuation-in-part of Ser. No. US 2001-920300, filed on 31 Jul 2001,

09567863

PENDING
PRAI US 2001-302051P 20010629 (60)
US 2001-279763P 20010328 (60)
US 2000-223283P 20000803 (60)
DT Utility
FS APPLICATION
LREP SEED INTELLECTUAL PROPERTY LAW GROUP PLLC, 701 FIFTH AVE, SUITE 6300, SEATTLE, WA, 98104-7092
CLMN Number of Claims: 17
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 8083
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Compositions and methods for the therapy and diagnosis of cancer, particularly colon cancer, are disclosed. Illustrative compositions comprise one or more colon tumor polypeptides, immunogenic portions thereof, polynucleotides that encode such polypeptides, antigen presenting cell that expresses such polypeptides, and T cells that are specific for cells expressing such polypeptides. The disclosed compositions are useful, for example, in the diagnosis, prevention and/or treatment of diseases, particularly colon cancer.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 5 OF 21 USPATFULL
AN 2002:51095 USPATFULL
TI Peptides comprising repetitive units of amino acids and DNA sequences encoding the same
IN Ferrari, Franco A., La Jolla, CA, United States
Richardson, Charles, Florence, MT, United States
Chambers, James, San Diego, CA, United States
Causey, Stuart, Palo Alto, CA, United States
Pollock, Thomas J., San Diego, CA, United States
Cappello, Joseph, San Diego, CA, United States
Crissman, John W., San Diego, CA, United States
PA Protein Polymer Technologies, Inc., San Diego, CA, United States (U.S. corporation)
PI US 6355776 B1 20020312
AI US 1999-444791 19991122 (9)
RLI Continuation of Ser. No. US 1995-482085, filed on 7 Jun 1995, now patented, Pat. No. US 6018030 Continuation-in-part of Ser. No. US 1993-175155, filed on 29 Dec 1993, now patented, Pat. No. US 5641648, issued on 24 Jun 1997 Continuation-in-part of Ser. No. US 1993-53049, filed on 22 Apr 1993, now abandoned Continuation of Ser. No. US 1987-114618, filed on 29 Oct 1987, now patented, Pat. No. US 5243038, issued on 7 Sep 1993 Continuation-in-part of Ser. No. US 1986-927258, filed on 4 Nov 1986, now abandoned
DT Utility
FS GRANTED
EXNAM Primary Examiner: McKelvey, Terry; Assistant Examiner: Sandals, William
LREP Flehr Hohbach Test Albritton & Herbert LLP, Trecartin, Esq., Richard F.
CLMN Number of Claims: 5
ECL Exemplary Claim: 1
DRWN 14 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 5152
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Novel polypeptides comprising repetitive units of amino acids, as well as synthetic genes encoding the subject polypeptides are provided. The subject polypeptides are characterized by comprising repetitive units of amino acids, where the repetitive units are present in naturally occurring proteins, particularly naturally occurring structural proteins. The subject polypeptides find use in a variety of

applications, such as structural components of prosthetic devices, synthetic fibers, and the like.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 6 OF 21 USPATFULL
AN 2001:226757 USPATFULL
TI Transferrin receptor reactive chimeric antibodies
IN Friden, Phillip M., Bedford, MA, United States
PA Alkermes, Inc., Cambridge, MA, United States (U.S. corporation)
PI US 6329508 B1 20011211
WO 9310819 19930610
AI US 1994-232246 19940705 (8)
WO 1992-US10206 19921124
19940705 PCT 371 date
19940705 PCT 102(e) date
RLI Continuation-in-part of Ser. No. US 1991-800458, filed on 26 Nov 1991, now abandoned Continuation-in-part of Ser. No. WO 1990-US5077, filed on 7 Sep 1990 Continuation-in-part of Ser. No. US 1989-404089, filed on 7 Sep 1989, now patented, Pat. No. US 5154924
DT Utility
FS GRANTED
EXNAM Primary Examiner: Huff, Sheela
LREP Hamilton Brook Smith & Reynolds, P.C.
CLMN Number of Claims: 4
ECL Exemplary Claim: 1
DRWN 79 Drawing Figure(s); 77 Drawing Page(s)
LN.CNT 1687
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention pertains to chimeric antibodies that are reactive with transferrin receptors on brain capillary endothelial cells. These antibodies are composed of a variable region, immunologically reactive with the transferrin receptors, that is obtained from one animal source, and a constant region that is derived from an animal source other than the one that provided the variable region. These chimeric antibodies can exist either as isolated entities or as conjugates with a neuropharmaceutical agent for transferal across the blood brain barrier.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 7 OF 21 USPATFULL
AN 2001:196825 USPATFULL
TI Complementary DNAs
IN Edwards, Jean-Baptiste Dumas Milne, Paris, France
Duclert, Aymeric, Saint Maur, France
Bougueleret, Lydie, Vanves, France
PA Genset, Paris, France (non-U.S. corporation)
PI US 6312922 B1 20011106
AI US 1999-247155 19990209 (9)
PRAI US 1998-74121P 19980209 (60)
US 1998-81563P 19980413 (60)
US 1998-96116P 19980810 (60)
US 1998-99273P 19980904 (60)
US 1998-96116P 19980904 (60)
US 1998-99273P 19980904 (60)
US 1998-99273P 19980904 (60)
US 1998-96116P 19980904 (60)
US 1998-99273P 19980904 (60)
US 1998-99273P 19980904 (60)
US 1998-99273P 19980904 (60)
DT Utility
FS GRANTED

09567863

EXNAM Primary Examiner: Brusca, John S.
LREP Knoibbe, Martens, Olson & Bear, LLP
CLMN Number of Claims: 33
ECL Exemplary Claim: 32
DRWN 12 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 6339
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The sequences of extended cDNAs encoding secreted proteins are disclosed. The extended cDNAs can be used to express secreted proteins or portions thereof or to obtain antibodies capable of specifically binding to the secreted proteins. The extended cDNAs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. The extended cDNAs may also be used to design expression vectors and secretion vectors.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 8 OF 21 USPATFULL
AN 2001:60048 USPATFULL
TI 5' ESTs for secreted proteins expressed in brain
IN Edwards, Jean-Baptiste Dumas Milne, Paris, France
Duclert, Aymeric, Saint Maur, France
Lacroix, Bruno, Saint-Genis Laval, France
PA Genset, Paris, France (non-U.S. corporation)
PI US 6222029 B1 20010424
AI US 1997-905223 19970801 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Priebe, Scott D.
LREP Knobbe Martens Olson & Bear LLP
CLMN Number of Claims: 20
ECL Exemplary Claim: 1,3,5,7,9
DRWN 7 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 4221
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The sequences of 5' ESTs derived from mRNAs encoding secreted proteins are disclosed. The 5' ESTs may be to obtain cDNAs and genomic DNAs corresponding to the 5' ESTs. The 5' ESTs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. Upstream regulatory sequences may also be otained using the 5' ESTs. The 5' ESTs may also be used to design expression vectors and secretion vectors.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 9 OF 21 USPATFULL
AN 2000:84062 USPATFULL
TI Isolated nucleic acid molecules encoding PARG, a GTPase activating protein which interacts with PTPL1
IN Saras, Jan, Uppsala, Sweden
Franzen, Petra, Uppsala, Sweden
Aspenstrom, Pontus, Uppsala, Sweden
Hellman, Ulf, Uppsala, Sweden
Gonez, Leonel Jorge, Hughesdale, Australia
Heldin, Carl-Henrik, Uppsala, Sweden
PA Ludwig Institute for Cancer Research, New York, NY, United States (U.S. corporation)
PI US 6083721 20000704
AI US 1998-80855 19980518 (9)
RLI Continuation-in-part of Ser. No. US 1997-805583, filed on 25 Feb 1997, now abandoned
DT Utility

09567863

FS Granted
EXNAM Primary Examiner: McKelvey, Terry
LREP Wolf, Greenfield & Sacks, P.C.
CLMN Number of Claims: 24
ECL Exemplary Claim: 1
DRWN 12 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 3145
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention describes nucleic acids encoding the PARG protein, including fragments and biologically functional variants thereof. Also included are polypeptides and fragments thereof encoded by such nucleic acids, and antibodies relating thereto. Methods and products for using such nucleic acids and polypeptides also are provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 10 OF 21 USPATFULL
AN 2000:10019 USPATFULL
TI Peptides comprising repetitive units of amino acids and DNA sequences encoding the same
IN Ferrari, Franco A., La Jolla, CA, United States
Richardson, Charles, Florence, MT, United States
Chambers, James, San Diego, CA, United States
Causey, Stuart, Palo Alto, CA, United States
Pollock, Thomas J., San Diego, CA, United States
Cappello, Joseph, San Diego, CA, United States
Crissman, John W., San Diego, CA, United States
PA Protein Polymer Technologies, Inc., San Diego, CA, United States (U.S. corporation)
PI US 6018030 20000125
AI US 1995-482085 19950607 (8)
RLI Continuation-in-part of Ser. No. US 1993-175155, filed on 29 Dec 1993, now patented, Pat. No. US 5641648 which is a continuation-in-part of Ser. No. US 1993-53049, filed on 22 Apr 1993, now abandoned which is a continuation of Ser. No. US 1987-114618, filed on 29 Oct 1987, now patented, Pat. No. US 5243038, issued on 7 Sep 1993 which is a continuation-in-part of Ser. No. US 1986-927258, filed on 4 Nov 1986, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Degen, Nancy; Assistant Examiner: Sandals, William
LREP Trecartin, Richard F.Flehr Hohbach Test Albritton & Herbert LLP
CLMN Number of Claims: 19
ECL Exemplary Claim: 1
DRWN 14 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 6111
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Polypeptides comprising repetitive units of amino acids, as well as synthetic genes encoding the subject polypeptides are provided. The subject polypeptides are characterized by comprising repetitive units of amino acids, where the repetitive units are present in naturally occurring proteins, particularly naturally occurring structural proteins. The subject polypeptides find use in a variety of applications, such as structural components of prosthetic devices, synthetic fibers, and the like.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 11 OF 21 USPATFULL
AN 2000:7057 USPATFULL
TI Transferrin receptor specific antibody-neuropharmaceutical or diagnostic agent conjugates

09567863

IN Friden, Phillip M., Bedford, MA, United States
PA Alkermes, Inc., Cambridge, MA, United States (U.S. corporation)
PI US 6015555 20000118
AI US 1995-444644 19950519 (8)
RLI Division of Ser. No. US 232246
DT Utility
FS Granted
EXNAM Primary Examiner: Burke, Julie
LREP Hamilton, Brook, Smith & Reynolds, P.C.
CLMN Number of Claims: 6
ECL Exemplary Claim: 1
DRWN 79 Drawing Figure(s); 77 Drawing Page(s)
LN.CNT 3966
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention pertains to a method for delivering a neuropharmaceutical or diagnostic agent across the blood brain barrier to the brain of a host. The method comprises administering to the host a therapeutically effective amount of an antibody-neuropharmaceutical or diagnostic agent conjugate wherein the antibody is reactive with a transferrin receptor and the antibody is a chimera between the variable region from one animal source and the constant region from a different animal source. Other aspects of this invention include a delivery system comprising an antibody reactive with a transferrin receptor linked to a neuropharmaceutical or diagnostic agent and methods for treating hosts afflicted with a disease associated with a neurological disorder.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 12 OF 21 USPATFULL
AN 1998:143904 USPATFULL
TI Directed evolution of novel binding proteins
IN Ladner, Robert Charles, Ijamsville, MD, United States
Gutterman, Sonia Kosow, Belmont, MA, United States
Roberts, Bruce Lindsay, Milford, MA, United States
Markland, William, Milford, MA, United States
Ley, Arthur Charles, Newton, MA, United States
Kent, Rachel Baribault, Boxborough, MA, United States
PA Dyax, Corp., Cambridge, MA, United States (U.S. corporation)
PI US 5837500 19981117
AI US 1995-415922 19950403 (8)
RLI Continuation of Ser. No. US 1993-9319, filed on 26 Jan 1993, now patented, Pat. No. US 5403484 which is a division of Ser. No. US 1991-664989, filed on 1 Mar 1991, now patented, Pat. No. US 5223409 which is a continuation-in-part of Ser. No. US 1990-487063, filed on 2 Mar 1990, now abandoned which is a continuation-in-part of Ser. No. US 1988-240160, filed on 2 Sep 1988, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Ulm, John
LREP Cooper, Iver P.
CLMN Number of Claims: 43
ECL Exemplary Claim: 1
DRWN 16 Drawing Figure(s); 16 Drawing Page(s)
LN.CNT 15973
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB In order to obtain a novel binding protein against a chosen target, DNA molecules, each encoding a protein comprising one of a family of similar potential binding domains and a structural signal calling for the display of the protein on the outer surface of a chosen bacterial cell, bacterial spore or phage (genetic package) are introduced into a genetic package. The protein is expressed and the potential binding domain is displayed on the outer surface of the package. The cells or viruses

bearing the binding domains which recognize the target molecule are isolated and amplified. The successful binding domains are then characterized. One or more of these successful binding domains is used as a model for the design of a new family of potential binding domains, and the process is repeated until a novel binding domain having a desired affinity for the target molecule is obtained. In one embodiment, the first family of potential binding domains is related to bovine pancreatic trypsin inhibitor, the genetic package is M13 phage, and the protein includes the outer surface transport signal of the M13 gene III protein.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 13 OF 21 USPATFULL
AN 1998:134864 USPATFULL
TI Methods for preparing synthetic repetitive DNA
IN Ferrari, Franco A., La Jolla, CA, United States
Cappello, Joseph, San Diego, CA, United States
Crissman, John W., San Diego, CA, United States
Dorman, Mary A., San Diego, CA, United States
PA Protein Polymer Technologies, Inc., San Diego, CA, United States (U.S. corporation)
PI US 5830713 19981103
AI US 1996-707237 19960903 (8)
RLI Continuation-in-part of Ser. No. US 1993-175155, filed on 29 Dec 1993, now patented, Pat. No. US 5641648 which is a continuation-in-part of Ser. No. US 1993-53049, filed on 22 Apr 1993, now abandoned which is a continuation-in-part of Ser. No. US 1990-609716, filed on 6 Nov 1990, now patented, Pat. No. US 5514581, issued on 7 May 1996 which is a continuation-in-part of Ser. No. US 1988-269429, filed on 9 Nov 1988, now abandoned which is a continuation-in-part of Ser. No. US 1987-114618, filed on 19 Oct 1987, now patented, Pat. No. US 5243038, issued on 7 Sep 1993 which is a continuation-in-part of Ser. No. US 1986-927258, filed on 4 Nov 1986, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Degen, Nancy
LREP Trecartin, Richard F., Kresnak, Mark T.Flehr Hohbach Test Albritton and Herbert
CLMN Number of Claims: 37
ECL Exemplary Claim: 1
DRWN 14 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 5084
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods are provided for the production of large polypeptides containing repeating sequences of amino acids utilizing biochemical techniques, specifically DNA sequences coding for the expression of the large polypeptides. Systems utilizing exogenous transcriptional and translational regions to control the production of the large polypeptides are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 14 OF 21 USPATFULL
AN 1998:88695 USPATFULL
TI DNA encoding recombinant lipoprotein antigens
IN Smith, Richard S., Del Mar, CA, United States
Curtiss, Linda K., San Diego, CA, United States
Koduri, Kanaka Raju, San Diego, CA, United States
Witztum, Joseph L., San Diego, CA, United States
Young, Stephen G., Hillsborough, CA, United States
PA The Scripps Research Institute, LaJolla, CA, United States (U.S.

corporation)
PI US 5786206 19980728
AI US 1994-333577 19941031 (8)
RLI Division of Ser. No. US 1992-959946, filed on 8 Oct 1992, now patented, Pat. No. US 5408038 which is a continuation-in-part of Ser. No. US 1992-901706, filed on 18 Jun 1992, now abandoned which is a continuation of Ser. No. US 1991-774633, filed on 9 Oct 1991, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Wax, Robert A.; Assistant Examiner: Lau, Kawai
LREP Welsh & Katz, Ltd.
CLMN Number of Claims: 12
ECL Exemplary Claim: 10
DRWN 7 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 3015
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods and compositions are described for determining the level of low density lipoproteins (LDL) in plasma. Native apoprotein B-100 (apo B-100) present in LDL particles is immunologically mimicked by a polypeptide of the invention. A polypeptide includes an amino acid residue sequence corresponding to a pan epitope region of the target apoprotein. A preferred polypeptide is a fusion protein that simultaneously mimics native apo B-100 and native apo A-I. Improved assay systems and methods for determining HDL and LDL levels in a body fluid sample are also described.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 15 OF 21 USPATFULL
AN 1998:72720 USPATFULL
TI Peptides comprising repetitive units of amino acids and DNA sequences encoding the same
IN Ferrari, Franco A., La Jolla, CA, United States
Richardson, Charles, Florence, MT, United States
Chambers, James, San Diego, CA, United States
Causey, Stuart, Palo Alto, CA, United States
Pollock, Thomas J., San Diego, CA, United States
Cappello, Joseph, San Diego, CA, United States
Crissman, John W., San Diego, CA, United States
PA Protein Polymer Technologies, Inc., San Diego, CA, United States (U.S. corporation)
PI US 5770697 19980623
AI US 1995-477509 19950607 (8)
RLI Continuation-in-part of Ser. No. US 1993-175155, filed on 29 Dec 1993, now patented, Pat. No. US 5641648, issued on 24 Jun 1997 which is a continuation-in-part of Ser. No. US 1993-53049, filed on 22 Apr 1993, now abandoned which is a continuation of Ser. No. US 1987-114618, filed on 29 Oct 1987, now patented, Pat. No. US 5243038, issued on 7 Sep 1993 which is a continuation-in-part of Ser. No. US 1986-927258, filed on 4 Nov 1986, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Ketter, James; Assistant Examiner: Brusca, John S.
LREP Trecartin, Richard F.
CLMN Number of Claims: 16
ECL Exemplary Claim: 1
DRWN 14 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 3242
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Novel polypeptides comprising repetitive units of amino acids, as well as synthetic genes encoding the subject polypeptides are provided. The subject polypeptides are characterized by comprising repetitive units of

amino acids, where the repetitive units are present in naturally occurring proteins, particularly naturally occurring structural proteins. The subject polypeptides find use in a variety of applications, such as structural components of prosthetic devices, synthetic fibers, and the like.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 16 OF 21 USPATFULL
AN 97:54100 USPATFULL
TI Methods for preparing synthetic repetitive DNA
IN Ferrari, Franco A., La Jolla, CA, United States
Cappello, Joseph, San Diego, CA, United States
Richardson, Charles, Florence, MT, United States
PA Protein Polymer Technologies, Inc., San Diego, CA, United States (U.S. corporation)
PI US 5641648 19970624
AI US 1993-175155 19931229 (8)
RLI Continuation-in-part of Ser. No. US 1993-53049, filed on 22 Apr 1993, now abandoned which is a continuation of Ser. No. US 1987-114618, filed on 29 Oct 1987, now patented, Pat. No. US 5243038 And a continuation-in-part of Ser. No. US 1990-609716, filed on 6 Nov 1990, now patented, Pat. No. US 5514581 which is a continuation-in-part of Ser. No. US 1988-269429, filed on 9 Nov 1988, now abandoned which is a continuation-in-part of Ser. No. US 1987-114618, filed on 29 Oct 1987, now patented, Pat. No. US 5243038 which is a continuation-in-part of Ser. No. US 1986-927258, filed on 4 Nov 1986, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Fleisher, Mindy; Assistant Examiner: Degen, Nancy J.
LREP Flehr Hohbach Test Albritton & Herbert LLP
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN 14 Drawing Figure(s); 10 Drawing Page(s)
LN.CNT 3033
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods are provided for the production of large polypeptides containing repeating sequences of amino acids utilizing biochemical techniques, specifically DNA sequences coding for the expression of the large polypeptides. Systems utilizing exogenous transcriptional and translational regions to control the production of the large polypeptides are also provided.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 17 OF 21 USPATFULL
AN 96:101466 USPATFULL
TI Directed evolution of novel binding proteins
IN Ladner, Robert C., Ijamsville, MD, United States
Guterman, Sonia K., Belmont, MA, United States
Roberts, Bruce L., Milford, MA, United States
Markland, William, Milford, MA, United States
Ley, Arthur C., Newton, MA, United States
Kent, Rachel B., Boxborough, MA, United States
PA Protein Engineering Corporation, Cambridge, MA, United States (U.S. corporation)
PI US 5571698 19961105
AI US 1993-57667 19930618 (8)
DCD 20100629
RLI Continuation of Ser. No. US 1991-664989, filed on 1 Mar 1991, now patented, Pat. No. US 5223409 which is a continuation-in-part of Ser. No. US 1990-487063, filed on 2 Mar 1990, now abandoned which is a

continuation-in-part of Ser. No. US 1988-240160, filed on 2 Sep 1988, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Ulm, John
LREP Cooper, Iver P.
CLMN Number of Claims: 83
ECL Exemplary Claim: 1
DRWN 16 Drawing Figure(s); 16 Drawing Page(s)
LN.CNT 15323
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB In order to obtain a novel binding protein against a chosen target, DNA molecules, each encoding a protein comprising one of a family of similar potential binding domains and a structural signal calling for the display of the protein on the outer surface of a chosen bacterial cell, bacterial spore or phage (genetic package) are introduced into a genetic package. The protein is expressed and the potential binding domain is displayed on the outer surface of the package. The cells or viruses bearing the binding domains which recognize the target molecule are isolated and amplified. The successful binding domains are then characterized. One or more of these successful binding domains is used as a model for the design of a new family of potential binding domains, and the process is repeated until a novel binding domain having a desired affinity for the target molecule is obtained. In one embodiment, the first family of potential binding domains is related to bovine pancreatic trypsin inhibitor, the genetic package is M13 phage, and the protein includes the outer surface transport signal of the M13 gene III protein.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 18 OF 21 USPATFULL
AN 95:34283 USPATFULL
TI Nonnatural apolipoprotein B-100 peptides and apolipoprotein B-100-apolipoprotein A-I fusion peptides
IN Smith, Richard S., Del Mar, CA, United States
Curtiss, Linda K., San Diego, CA, United States
Koduri, Kanaka R., San Diego, CA, United States
Witztum, Joseph L., San Diego, CA, United States
Young, Stephen G., Hillsborough, CA, United States
PA The Scripps Research Institute, La Jolla, CA, United States (U.S. corporation)
PI US 5408038 19950418
AI US 1992-959946 19921008 (7)
RLI Continuation-in-part of Ser. No. US 1992-901706, filed on 18 Jun 1992, now abandoned which is a continuation of Ser. No. US 1991-774633, filed on 9 Oct 1991, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Parr, Margaret; Assistant Examiner: Schreiber, David
LREP Welsh & Katz
CLMN Number of Claims: 12
ECL Exemplary Claim: 1
DRWN 7 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 2961
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods and compositions are described for determining the level of low density lipoproteins (LDL) in plasma. Native apoprotein B-100 (apo B-100) present in LDL particles is immunologically mimicked by a polypeptide of the invention. A polypeptide includes an amino acid residue sequence corresponding to a pan epitope region of the target apoprotein. A preferred polypeptide is a fusion protein that

simultaneously mimics native apo B-100 and native apo A-I. Improved assay systems and methods for determining HDL and LDL levels in a body fluid sample are also described.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 19 OF 21 USPATFULL
AN 95:29292 USPATFULL
TI Viruses expressing chimeric binding proteins
IN Ladner, Robert C., Ijamsville, MD, United States
Guterman, Sonia K., Belmont, MA, United States
Roberts, Bruce L., Milford, MA, United States
Markland, William, Milford, MA, United States
Ley, Arthur C., Newton, MA, United States
Kent, Rachel B., Boxborough, MA, United States
PA Protein Engineering Corporation, Cambridge, MA, United States (U.S. corporation)
PI US 5403484 19950404
AI US 1993-9319 19930126 (8)
RLI Division of Ser. No. US 1991-664989, filed on 1 Mar 1991, now patented, Pat. No. US 5223409 which is a continuation-in-part of Ser. No. US 1990-487063, filed on 2 Mar 1990, now abandoned which is a continuation-in-part of Ser. No. US 1988-240160, filed on 2 Sep 1988, now abandoned
PRAI WO 1989-3731 19890901
DT Utility
FS Granted
EXNAM Primary Examiner: Hill, Jr., Robert J.; Assistant Examiner: Ulm, John D.
LREP Cooper, Iver P.
CLMN Number of Claims: 49
ECL Exemplary Claim: 1
DRWN 16 Drawing Figure(s); 16 Drawing Page(s)
LN.CNT 14368
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB In order to obtain a novel binding protein against a chosen target, DNA molecules, each encoding a protein comprising one of a family of similar potential binding domains and a structural signal calling for the display of the protein on the outer surface of a chosen bacterial cell, bacterial spore or phage (genetic package) are introduced into a genetic package. The protein is expressed and the potential binding domain is displayed on the outer surface of the package. The cells or viruses bearing the binding domains which recognize the target molecule are isolated and amplified. The successful binding domains are then characterized. One or more of these successful binding domains is used as a model for the design of a new family of potential binding domains, and the process is repeated until a novel binding domain having a desired affinity for the target molecule is obtained. In one embodiment, the first family of potential binding domains is related to bovine pancreatic trypsin inhibitor, the genetic package is M13 phage, and the protein includes the outer surface transport signal of the M13 gene III protein.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 20 OF 21 USPATFULL
AN 93:52487 USPATFULL
TI Directed evolution of novel binding proteins
IN Ladner, Robert C., Ijamsville, MD, United States
Guterman, Sonia K., Belmont, MA, United States
Roberts, Bruce L., Milford, MA, United States
Markland, William, Milford, MA, United States
Ley, Arthur C., Newton, MA, United States

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Kent, Rachel B., Boxborough, MA, United States
PA Protein Engineering Corp., Cambridge, MA, United States (U.S. corporation)
PI US 5223409 19930629
AI US 1991-664989 19910301 (7)
RLI Continuation-in-part of Ser. No. US 1990-487063, filed on 2 Mar 1990, now abandoned And a continuation-in-part of Ser. No. US 1988-240160, filed on 2 Sep 1988, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Hill, Jr., Robert J.; Assistant Examiner: Ulm, John D.
LREP Cooper, Iver P.
CLMN Number of Claims: 66
ECL Exemplary Claim: 1
DRWN 16 Drawing Figure(s); 16 Drawing Page(s)
LN.CNT 15410
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB In order to obtain a novel binding protein against a chosen target, DNA molecules, each encoding a protein comprising one of a family of similar potential binding domains and a structural signal calling for the display of the protein on the outer surface of a chosen bacterial cell, bacterial spore or phage (genetic package) are introduced into a genetic package. The protein is expressed and the potential binding domain is displayed on the outer surface of the package. The cells or viruses bearing the binding domains which recognize the target molecule are isolated and amplified. The successful binding domains are then characterized. One or more of these successful binding domains is used as a model for the design of a new family of potential binding domains, and the process is repeated until a novel binding domain having a desired affinity for the target molecule is obtained. In one embodiment, the first family of potential binding domains is related to bovine pancreatic trypsin inhibitor, the genetic package is M13 phage, and the protein includes the outer surface transport signal of the M13 gene III protein.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L24 ANSWER 21 OF 21 USPATFULL
AN 90:48734 USPATFULL
TI Expression of higher eucaryotic genes in aspergillus
IN McKnight, Gary L., Seattle, WA, United States
Upshall, Alan, Bothell, WA, United States
PA ZymoGenetics, Inc., Seattle, WA, United States (U.S. corporation)
PI US 4935349 19900619
AI US 1987-946873 19870109 (6)
RLI Continuation-in-part of Ser. No. US 1986-820519, filed on 17 Jan 1986, now abandoned
DT Utility
FS Granted
EXNAM Primary Examiner: Weimar, Elizabeth C.; Assistant Examiner: Peet, Richard C.
LREP Seed and Berry
CLMN Number of Claims: 10
ECL Exemplary Claim: 8
DRWN 33 Drawing Figure(s); 28 Drawing Page(s)
LN.CNT 1406
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method for expressing higher eucaryotic genes in Aspergillus through the use of a recombinant plasmid capable of integration into the chromosomal DNA of Aspergillus is disclosed. It is preferred to utilize a transcriptional promoter within a DNA construct contained in the plasmid that is of a DNA sequence encoding an ADH enzyme or a TPI

enzyme. Promoters capable of directing the expression of a heterologous gene in Aspergillus, as well as other filamentous fungal genera are also disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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d his

(FILE 'HOME' ENTERED AT 10:12:59 ON 18 DEC 2002)

FILE 'BIOSIS, MEDLINE, CAPLUS, WPIDS, USPATFULL' ENTERED AT 10:13:34 ON 18 DEC 2002

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L1        343861 S NUCLEIC ACID
L2             2 S L1 AND POSITIV? (3A) CHARGE TAG (3A) NUCLEIC ACID?
L3            21 S L1 AND POSITIV? (4A) CHARG? (3A) TAG?
L4            19 S L3 NOT L2
L5            19 DUP REM L4 (0 DUPLICATES REMOVED)
L6           109 S L1 AND POSITIV? (4A) LABEL
L7           108 S L6 NOT L5
L8            92 S L7 AND PHOSPHAT?
L9            92 DUP REM L8 (0 DUPLICATES REMOVED)
L10           22 S L9 AND POSITIV? (4A) CHARG?
L11            1 S POSITIV? (3A) CHARG? (3A) LABEL? (4A) TERMINAL (4A) (NUCLEIC
L12            1 S L11 AND POSITIV?
L13          110 S MASS TAG
L14           50 S L13 AND OLIGONUCLEOTIDE?
L15           43 S L14 AND LABEL?
L16           21 S L15 AND TERMINAL
L17           21 DUP REM L16 (0 DUPLICATES REMOVED)
L18            1 S POSITIV? CHARG? LABEL? OLIGONUCLEOTIDE?
L19            1 S POSITIV? (4A) CHARG? LABEL? (3A) OLIGONUCLEOTIDE?
L20          117 S POSITIV? (5A) (LABEL? OR TAG?) (4A) OLIGONUCLEOTIDE?
L21           31 S L20 AND AMINE
L22           23 S L21 AND AMMONIUM
L23            2 S L22 AND PHOSPHORAMIDITE
L24           21 S L22 NOT L23
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=> d l28 bib abs 1-16

L28 ANSWER 1 OF 16 WPIDS (C) 2002 THOMSON DERWENT
AN 2002-075320 [10] WPIDS
DNC C2002-022504
TI Detecting **nucleic acid** e.g. for detecting single nucleotide polymorphisms by fluorescence hybridization involves use of **nucleic acid** probes comprising neutral or positively charged fluorescent label.
DC B04 D16
IN JEONG, S; NIKIFOROV, T T
PA (CALI-N) CALIPER TECHNOLOGIES CORP; (JEON-I) JEONG S; (NIKI-I) NIKIFOROV T T
CYC 23
PI WO 2001088195 A1 20011122 (200210)* EN 69p
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR
W: AU CA JP
AU 2001061523 A 20011126 (200222)
US 2002037520 A1 20020328 (200225)
ADT WO 2001088195 A1 WO 2001-US15427 20010511; AU 2001061523 A AU 2001-61523 20010511; US 2002037520 A1 Provisional US 2000-203723P 20000512, US 2001-854417 20010511
FDT AU 2001061523 A Based on WO 200188195
PRAI US 2000-203723P 20000512; US 2001-854417 20010511
AN 2002-075320 [10] WPIDS
AB WO 200188195 A UPAB: 20020213
NOVELTY - Detecting (M1) **nucleic acid**, comprising contacting first **nucleic acid** to second **nucleic acid** which comprises neutral or positively charged fluorescent label, and detecting fluorescence polarization (FP) of the resulting mixture of first and second nucleic acids, is new.
DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:
(1) a system (I) comprising:
(a) a container having a duplexed **nucleic acid**, where at least one strand of the **nucleic acid** duplex has a neutral or positively charged fluorescent label;
(b) a polarized light source positioned to shine plant polarized light through a portion of the container, thereby exciting the fluorescent label during operation of the system; and
(c) a detector that detects resultant polarization of light emitted by the fluorescent label;
(2) a microfluidic fluorescent polarization **nucleic acid** analysis system, comprising:
(a) a microfluidic device comprising a body structure having at least two microfluidic channels disposed in it;
(b) a source of a first **nucleic acid**;
(c) a source of a second **nucleic acid** comprises a neutral or positively charged fluorescent label;
(d) a source of plane polarized light, which source is positioned to illuminate a portion of at lest one of the least two microchannels; and
(e) a fluorescence polarization detector positioned to detect plane polarized light emitted form the microfluidic device; and
(3) a computer implemented process in an assay system for quantifying **nucleic acid** hybridization parameter, where the assay system involves:
(a) providing first **nucleic acid** composition comprising first **nucleic acid** having positive or neutral fluorescent label;
(b) introducing second **nucleic acid** into first **nucleic acid** composition to provide a second

nucleic acid composition, the second **nucleic acid** reacting with the first **nucleic acid** to produce a fluorescently labeled product having a substantially different rotation rate than the first **nucleic acid**;

(c) determining a first level of fluorescence polarization of the first **nucleic acid** composition;

(d) determining a second level of fluorescence polarization of the second **nucleic acid** composition;

(e) comparing the first and second levels of fluorescent polarization; and

(f) calculating the **nucleic acid** hybridization parameter.

USE - Detecting a **nucleic acid** by contacting first **nucleic acid** such as DNA, RNA, LNA (locked **nucleic acid**), DNA or RNA analog, or peptide **nucleic acid** (PNA). (M1) is useful for identifying the presence of a subsequence of nucleotides in a target **nucleic acid**, comprising contacting target **nucleic acid** with a labeled **nucleic acid** probe that comprises a neutral or **positively charged label** comprising a fluorophore to form a first reaction mixture, and detecting the level of FP of first reaction mixture. The target **nucleic acid** sequences comprises at least one locus for single nucleotide polymorphism (SNP) and the **nucleic acid** probe is complementary to one allele of SNP in the target **nucleic acid** sequence. Optionally, the method preferably involves contacting several additional target nucleic acids with several additional **nucleic acid** probes, each of which comprises a neutral or **positively charged label** comprising a fluorophore to form several additional reaction mixture, and detecting the level of FP of several additional reaction mixture. Each of the additional target **nucleic acid** comprises a locus for SNP and each of the several additional probes are complementary to at least one allele of each of the SNPs in the target **nucleic acid** sequences derived from a single species, variety, cultivar, cell, virus, or organism. The identification of SNPs provides a SNP genotype for the species, variety, cultivar, cell, virus or organism. (All claimed). (M1) is useful for detecting single nucleotide polymorphisms and in a method of genotyping a **nucleic acid** sample. The microfluidic devices are useful for performing high throughput screening assays in drug discovery, immunoassays, diagnostics, and genetic analysis.

ADVANTAGE - The method is simple, and is less biased. The use of neutral or positively charged fluorescent labels on **nucleic acid** probes results in a relatively large change in observed FP of the probe labeled during **nucleic acid** hybridization. Preferably, addition of polylysine (a positively charged linker) to first and second nucleic acids increases FP by less than 50 %.

Dwg.0/12

L28 ANSWER 2 OF 16 USPATFULL
AN 2002:329806 USPATFULL
TI Invasion assays
IN Hall, Jeff G., Madison, WI, UNITED STATES
Lyamichev, Victor I., Madison, WI, UNITED STATES
Mast, Andrea L., Madison, WI, UNITED STATES
Brow, Mary Ann D., Madison, WI, UNITED STATES
PI US 2002187486 A1 20021212
AI US 2001-33297 A1 20011102 (10)
RLI Continuation of Ser. No. US 1999-350597, filed on 9 Jul 1999, PENDING Continuation of Ser. No. US 1997-823516, filed on 24 Mar 1997, GRANTED, Pat. No. US 5994069 Continuation-in-part of Ser. No. US 1996-756038, filed on 26 Nov 1996, ABANDONED Continuation-in-part of Ser. No. US

1996-756386, filed on 26 Nov 1996, GRANTED, Pat. No. US 5985557 Continuation-in-part of Ser. No. US 1996-682853, filed on 12 Jul 1996, GRANTED, Pat. No. US 6001567 Continuation-in-part of Ser. No. US 1996-599491, filed on 24 Jan 1996, GRANTED, Pat. No. US 5846717
DT Utility
FS APPLICATION
LREP MEDLEN & CARROLL, LLP, Suite 350, 101 Howard Street, San Francisco, CA, 94105
CLMN Number of Claims: 34
ECL Exemplary Claim: 1
DRWN 121 Drawing Page(s)
LN.CNT 10560
AB The present invention relates to means for the detection and characterization of **nucleic acid** sequences, as well as variations in **nucleic acid** sequences. The present invention also relates to methods for forming a **nucleic acid** cleavage structure on a target sequence and cleaving the **nucleic acid** cleavage structure in a site-specific manner. The structure-specific nuclease activity of a variety of enzymes is used to cleave the target-dependent cleavage structure, thereby indicating the presence of specific **nucleic acid** sequences or specific variations thereof. The present invention further relates to methods and devices for the separation of **nucleic acid** molecules based on charge. The present invention also provides methods for the detection of non-target cleavage products via the formation of a complete and activated protein binding region. The invention further provides sensitive and specific methods for the detection of human cytomegalovirus **nucleic acid** in a sample.

L28 ANSWER 3 OF 16 USPATFULL
AN 2002:254176 USPATFULL
TI Detection of nucleic acids by multiple sequential invasive cleavages 02
IN Hall, Jeff G., Madison, WI, United States
Lyamichev, Victor I., Madison, WI, United States
Mast, Andrea L., Madison, WI, United States
Brow, Mary Ann D., Madison, WI, United States
PA Third Wave Technologies, Inc, Madison, WI, United States (U.S. corporation)
PI US 6458535 B1 20021001
AI US 1999-350597 19990709 (9)
RLI Continuation of Ser. No. US 1997-823516, filed on 24 Mar 1997, now patented, Pat. No. US 5994069 Continuation-in-part of Ser. No. US 1996-759038, filed on 2 Dec 1996, now patented, Pat. No. US 6090543 Continuation-in-part of Ser. No. US 1996-756386, filed on 26 Nov 1996, now patented, Pat. No. US 5085557 Continuation-in-part of Ser. No. US 1996-682853, filed on 12 Jul 1996, now patented, Pat. No. US 6001567 Continuation-in-part of Ser. No. US 1996-599491, filed on 24 Jan 1996, now patented, Pat. No. US 5846717, issued on 8 Dec 1998
DT Utility
FS GRANTED
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Souaya, Jehanne
LREP Medlen & Carroll, LLP
CLMN Number of Claims: 27
ECL Exemplary Claim: 1
DRWN 170 Drawing Figure(s); 128 Drawing Page(s)
LN.CNT 13831
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to means for the detection and characterization of **nucleic acid** sequences, as well as variations in **nucleic acid** sequences. The present

invention also relates to methods for forming a **nucleic acid** cleavage structure on a target sequence and cleaving the **nucleic acid** cleavage structure in a site-specific manner. The structure-specific nuclease activity of a variety of enzymes is used to cleave the target-dependent cleavage structure, thereby indicating the presence of specific **nucleic acid** sequences or specific variations thereof. The present invention further relates to methods and devices for the separation of **nucleic acid** molecules based on charge. The present invention also provides methods for the detection of non-target cleavage products via the formation of a complete and activated protein binding region. The invention further provides sensitive and specific methods for the detection of human cytomegalovirus **nucleic acid** in a sample.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L28 ANSWER 4 OF 16 USPATFULL
AN 2002:236261 USPATFULL
TI Charge tags and the separation of **nucleic acid** molecules
IN Lyamichev, Victor, Madison, WI, UNITED STATES
Skrzpczynski, Zbigniew, Verona, WI, UNITED STATES
Allawi, Hatim T., Madison, WI, UNITED STATES
Wayland, Sarah R., Madison, WI, UNITED STATES
Takova, Tsetska, Madison, WI, UNITED STATES
Neri, Bruce P., Madison, WI, UNITED STATES
PA Third Wave Technologies, Inc. (U.S. corporation)
PI US 2002128465 A1 20020912
AI US 2001-777430 A1 20010206 (9)
RLI Continuation-in-part of Ser. No. US 1999-333145, filed on 14 Jun 1999, PENDING Continuation-in-part of Ser. No. US 1996-682853, filed on 12 Jul 1996, GRANTED, Pat. No. US 6001567
DT Utility
FS APPLICATION
LREP MEDLEN & CARROLL, LLP, 101 HOWARD STREET, SUITE 350, SAN FRANCISCO, CA, 94105
CLMN Number of Claims: 86
ECL Exemplary Claim: 1
DRWN 46 Drawing Page(s)
LN.CNT 5163
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to novel phosphoramidites, including positive and neutrally charged compounds. The present invention also provides charge tags for attachment to materials including solid supports and nucleic acids, wherein the charge tags increase or decrease the net charge of the material. The present invention further provides methods for separating and characterizing molecules based on the charge differentials between modified and unmodified materials.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L28 ANSWER 5 OF 16 USPATFULL
AN 2002:66867 USPATFULL
TI Detection of **nucleic acid** hybridization by fluorescence polarization
IN Nikiforov, Theo T., San Jose, CA, UNITED STATES
Jeong, Sang, Mountain View, CA, UNITED STATES
PI US 2002037520 A1 20020328
AI US 2001-854417 A1 20010511 (9)
PRAI US 2000-203723P 20000512 (60)
DT Utility

09567863

FS APPLICATION
LREP LAW OFFICES OF JONATHAN ALAN QUINE, P O BOX 458, ALAMEDA, CA, 94501
CLMN Number of Claims: 52
ECL Exemplary Claim: 1
DRWN 21 Drawing Page(s)
LN.CNT 1793
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods, systems and assays are provided for FP detection of **nucleic acid** hybridization.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L28 ANSWER 6 OF 16 USPATFULL
AN 2002:34297 USPATFULL
TI Invasive cleavage of nucleic acids
IN Prudent, James R., Madison, WI, United States
Hall, Jeff G., Madison, WI, United States
Lyamichev, Victor I., Madison, WI, United States
Brow, Mary Ann D., Madison, WI, United States
Dahlberg, James E., Madison, WI, United States
PA Third Wave Technologies, Inc., Madison, WI, United States (U.S. corporation)
PI US 6348314 B1 20020219
AI US 1999-350309 19990709 (9)
RLI Division of Ser. No. US 1996-756386, filed on 29 Nov 1996, now patented, Pat. No. US 5985557 Continuation-in-part of Ser. No. US 1996-682853, filed on 12 Jul 1996, now patented, Pat. No. US 6001567 Continuation-in-part of Ser. No. US 1996-599491, filed on 24 Jan 1996, now patented, Pat. No. US 5846717, issued on 8 Dec 1998
DT Utility
FS GRANTED
EXNAM Primary Examiner: Campbell, Eggerton A.
LREP Medlen & Carroll, LLP
CLMN Number of Claims: 72
ECL Exemplary Claim: 1
DRWN 118 Drawing Figure(s); 90 Drawing Page(s)
LN.CNT 8623
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to means for the detection and characterization of **nucleic acid** sequences, as well as variations in **nucleic acid** sequences. The present invention also relates to methods for forming a **nucleic acid** cleavage structure on a target sequence and cleaving the **nucleic acid** cleavage structure in a site-specific manner. The structure-specific nuclease activity of a variety of enzymes is used to cleave the target-dependent cleavage structure, thereby indicating the presence of specific **nucleic acid** sequences or specific variations thereof.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L28 ANSWER 7 OF 16 USPATFULL
AN 2001:202592 USPATFULL
TI Modified ligands of calcium-dependent binding proteins
IN Neri, Dario, Zurich, Switzerland
Winter, Gregory Paul, Cambridge, United Kingdom
PA Medical Research Council, London, United Kingdom (non-U.S. corporation)
PI US 6316409 B1 20011113
WO 9740142 19971030
AI US 1999-142356 19990303 (9)
WO 1997-GB1152 19970425
19990303 PCT 371 date

09567863

19990303 PCT 102(e) date
PRAI GB 1996-8510 19960425
DT Utility
FS GRANTED
EXNAM Primary Examiner: Low, Christopher S. F.; Assistant Examiner: Tu, Stephen
LREP Darby & Darby
CLMN Number of Claims: 19
ECL Exemplary Claim: 1
DRWN 3 Drawing Figure(s); 3 Drawing Page(s)
LN.CNT 814
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to ligands capable of binding a calcium dependent binding protein, that comprise an amino acid sequence corresponding to that of a wild type ligand for the calcium dependent binding protein with modification which results in enhanced affinity of the ligand for the calcium dependent binding protein.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L28 ANSWER 8 OF 16 USPATFULL
AN 2001:157679 USPATFULL
TI Systems for electrophoretic transport and detection of analytes
IN Kayyem, Jon Faiz, Pasadena, CA, United States
Blackburn, Gary, Glendora, CA, United States
O'Connor, Stephen D., Pasadena, CA, United States
PA Clinical Micro Sensors, Inc., Pasadena, CA, United States (U.S. corporation)
PI US 6290839 B1 20010918
AI US 1998-134058 19980814 (9)
PRAI US 1998-90389P 19980623 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Tung, T.; Assistant Examiner: Noguerola, Alex
LREP Flehr Hohbach Test Albritton & Herbert LLP, Trecartin, Esq., Richard F., Silva, Esq., Robin M.
CLMN Number of Claims: 28
ECL Exemplary Claim: 1
DRWN 44 Drawing Figure(s); 21 Drawing Page(s)
LN.CNT 4594
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to compositions and methods useful in the electrophoretic transport of target analytes to a detection electrode comprising a self-assembled monolayer (SAM). Detection proceeds through the use of an electron transfer moiety (ETM) that is associated with the target analyte, either directly or indirectly, to allow electronic detection of the ETM.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L28 ANSWER 9 OF 16 USPATFULL
AN 2001:116434 USPATFULL
TI Binding acceleration techniques for the detection of analytes
IN Blackburn, Gary, Glendora, CA, United States
Creager, Stephen E., Central, SC, United States
Fraser, Scott, La Canada, CA, United States
Irvine, Bruce D., Glendora, CA, United States
Meade, Thomas J., Altadena, CA, United States
O'Connor, Stephen D., Pasadena, CA, United States
Terbrueggen, Robert H., Manhattan Beach, CA, United States
Vielmetter, Jost G., Pasadena, CA, United States
Welch, Thomas W., Pasadena, CA, United States

09567863

PA Clinical Micro Sensors, Inc., Pasadena, CA, United States (U.S. corporation)
PI US 6264825 B1 20010724
AI US 1999-338726 19990623 (9)
RLI Continuation of Ser. No. US 1998-134058, filed on 14 Aug 1998
PRAI US 1998-90389P 19980623 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Tung, T.; Assistant Examiner: Noguerola, Alex
LREP Flehr Hohabch Test Albritton & Herbert LLP, Trecartin, Esq., Richard F., Silva, Esq., Robin M.
CLMN Number of Claims: 29
ECL Exemplary Claim: 1
DRWN 49 Drawing Figure(s); 22 Drawing Page(s)
LN.CNT 5644
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention relates to compositions and methods useful in the acceleration of binding of target analytes to capture ligands on surfaces. Detection proceeds through the use of an electron transfer moiety (ETM) that is associated with the target analyte, either directly or indirectly, to allow electronic detection of the ETM.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L28 ANSWER 10 OF 16 USPATFULL
AN 2000:91761 USPATFULL
TI Cleavage agents
IN Kaiser, Michael W., Madison, WI, United States
Lyamichev, Victor I., Madison, WI, United States
Lyamicheva, Natasha, Madison, WI, United States
PA Third Wave Technologies, Inc., Madison, WI, United States (U.S. corporation)
PI US 6090606 20000718
AI US 1996-758314 19961202 (8)
RLI Continuation-in-part of Ser. No. US 1996-756386, filed on 26 Nov 1996 which is a continuation-in-part of Ser. No. US 1996-682853, filed on 12 Jul 1996 which is a continuation-in-part of Ser. No. US 1996-599491, filed on 24 Jan 1996, now patented, Pat. No. US 5846717 which is a continuation-in-part of Ser. No. US 1996-756376, filed on 2 Dec 1996
DT Utility
FS Granted
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Shoemaker, Debra
LREP Medlen & Carroll, LLP
CLMN Number of Claims: 24
ECL Exemplary Claim: 6
DRWN 144 Drawing Figure(s); 117 Drawing Page(s)
LN.CNT 11295
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to means for the detection and characterization of **nucleic acid** sequences, as well as variations in **nucleic acid** sequences. The present invention also relates to improved cleavage means for the detection and characterization of **nucleic acid** sequences. Structure-specific nucleases derived from a variety of thermostabe organisms are provided. These structure-specific nucleases are used to cleave target-dependent cleavage structures, thereby indicating the presence of specific **nucleic acid** sequences or specific variations thereof.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L28 ANSWER 11 OF 16 USPATFULL

09567863

AN 2000:91698 USPATFULL
TI Cleavage of nucleic acids
IN Prudent, James R., Madison, WI, United States
Hall, Jeff G., Madison, WI, United States
Lyamichev, Victor I., Madison, WI, United States
Brow, Mary Ann D., Madison, WI, United States
Dahlberg, James E., Madison, WI, United States
PA Third Wave Technologies, Inc., Madison, WI, United States (U.S. corporation)
PI US 6090543 20000718
AI US 1996-759038 19961202 (8)
RLI Continuation-in-part of Ser. No. US 1996-756386, filed on 26 Nov 1996 which is a continuation-in-part of Ser. No. US 1996-682853, filed on 12 Jul 1996 which is a continuation-in-part of Ser. No. US 1996-599491, filed on 24 Jan 1996 76 Ser. No. US 1996-758314, filed on 2 Dec 1996
DT Utility
FS Granted
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Shoemaker, Debra
LREP Medlen & Carroll, LLP
CLMN Number of Claims: 27
ECL Exemplary Claim: 1
DRWN 102 Drawing Figure(s); 117 Drawing Page(s)
LN.CNT 11426
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to means for the detection and characterization of **nucleic acid** sequences, as well as variations in **nucleic acid** sequences. The present invention also relates to methods for forming a **nucleic acid** cleavage structure on a target sequence and cleaving the **nucleic acid** cleavage structure in a site-specific manner. The structure-specific nuclease activity of a variety of enzymes is used to cleave the target-dependent cleavage structure, thereby indicating the presence of specific **nucleic acid** sequences or specific variations thereof.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L28 ANSWER 12 OF 16 USPATFULL
AN 1999:163423 USPATFULL
TI Detection of **nucleic acid** sequences by invader-directed cleavage
IN Brow, Mary Ann D., Madison, WI, United States
Hall, Jeff Steven Groteluesch en, Madison, WI, United States
Lyamichev, Victor, Madison, WI, United States
Olive, David Michael, Madison, WI, United States
Prudent, James Robert, Madison, WI, United States
PA Third Wave Technologies, Inc., CA, United States (U.S. corporation)
PI US 6001567 19991214
AI US 1996-682853 19960712 (8)
RLI Continuation-in-part of Ser. No. US 1996-599491, filed on 24 Jan 1996, now patented, Pat. No. US 5846717
DT Utility
FS Granted
EXNAM Primary Examiner: Arthur, Lisa B.; Assistant Examiner: Souaya, Jehanne
LREP Medlen & Carroll, LLP
CLMN Number of Claims: 15
ECL Exemplary Claim: 1
DRWN 66 Drawing Figure(s); 82 Drawing Page(s)
LN.CNT 7836
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to means for the detection and characterization of **nucleic acid** sequences, as well

as variations in **nucleic acid** sequences. The present invention also relates to methods for forming a **nucleic acid** cleavage structure on a target sequence and cleaving the **nucleic acid** cleavage structure in a site-specific manner. The 5' nuclease activity of a variety of enzymes is used to cleave the target-dependent cleavage structure, thereby indicating the presence of specific **nucleic acid** sequences or specific variations thereof. The present invention further relates to methods and devices for the separation of **nucleic acid** molecules based by charge.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L28 ANSWER 13 OF 16 USPATFULL
AN 1999:155453 USPATFULL
TI Detection of nucleic acids by multiple sequential invasive cleavages
IN Hall, Jeff G., Madison, WI, United States
Lyamichev, Victor I., Madison, WI, United States
Mast, Andrea L., Madison, WI, United States
Brow, Mary Ann D., Madison, WI, United States
PA Third Wave Technologies, Inc., Madison, WI, United States (U.S. corporation)
PI US 5994069 19991130
AI US 1997-823516 19970324 (8)
RLI Continuation-in-part of Ser. No. WO 1997-US1072, filed on 21 Jan 1997 which is a continuation-in-part of Ser. No. US 1996-759038, filed on 2 Dec 1996 And a continuation-in-part of Ser. No. US 1996-758314, filed on 2 Dec 1996 which is a continuation-in-part of Ser. No. US 1996-756386, filed on 26 Nov 1996 which is a continuation-in-part of Ser. No. US 1996-682853, filed on 12 Jul 1996 which is a continuation-in-part of Ser. No. US 1996-599491, filed on 24 Jan 1996 , said Ser. No. US 759038 which is a continuation-in-part of Ser. No. US 1996-756386, filed on 26 Nov 1996
DT Utility
FS Granted
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Shoemaker, Debra
LREP Medlen & Carroll, LLP
CLMN Number of Claims: 34
ECL Exemplary Claim: 1
DRWN 169 Drawing Figure(s); 128 Drawing Page(s)
LN.CNT 14892
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to means for the detection and characterization of **nucleic acid** sequences, as well as variations in **nucleic acid** sequences. The present invention also relates to methods for forming a **nucleic acid** cleavage structure on a target sequence and cleaving the **nucleic acid** cleavage structure in a site-specific manner. The structure-specific nuclease activity of a variety of enzymes is used to cleave the target-dependent cleavage structure, thereby indicating the presence of specific **nucleic acid** sequences or specific variations thereof. The present invention further relates to methods and devices for the separation of **nucleic acid** molecules based on charge. The present invention also provides methods for the detection of non-target cleavage products via the formation of a complete and activated protein binding region. The invention further provides sensitive and specific methods for the detection of human cytomegalovirus **nucleic acid** in a sample.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

09567863

L28 ANSWER 14 OF 16 USPATFULL
AN 1999:146257 USPATFULL
TI Invasive cleavage of nucleic acids
IN Prudent, James R., Madison, WI, United States
Hall, Jeff G., Madison, WI, United States
Lyamichev, Victor I., Madison, WI, United States
Brow, Mary Ann D., Madison, WI, United States
Dahlberg, James E., Madison, WI, United States
PA Third Wave Technologies, Inc., WI, United States (U.S. corporation)
PI US 5985557 19991116
AI US 1996-756386 19961126 (8)
RLI Continuation-in-part of Ser. No. US 1996-682853, filed on 12 Jul 1996 which is a continuation-in-part of Ser. No. US 1996-599491, filed on 24 Jan 1996, now patented, Pat. No. US 5846717
DT Utility
FS Granted
EXNAM Primary Examiner: Campbell, Eggerton A.
LREP Medlen & Carroll, LLP
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN 87 Drawing Figure(s); 90 Drawing Page(s)
LN.CNT 8630
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to means for the detection and characterization of **nucleic acid** sequences, as well as variations in **nucleic acid** sequences. The present invention also relates to methods for forming a **nucleic acid** cleavage structure on a target sequence and cleaving the **nucleic acid** cleavage structure in a site-specific manner. The structure-specific nuclease activity of a variety of enzymes is used to cleave the target-dependent cleavage structure, thereby indicating the presence of specific **nucleic acid** sequences or specific variations thereof.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L28 ANSWER 15 OF 16 USPATFULL
AN 1998:17197 USPATFULL
TI Labeled complex and method of analysis therewith
IN Miyazaki, Takeshi, Ebina, Japan
Okamoto, Tadashi, Yokohama, Japan
Tanaka, Kazumi, Yokohama, Japan
Onishi, Toshikazu, Machida, Japan
Fukui, Tetsuro, Yokohama, Japan
Yamamoto, Nobuko, Isehara, Japan
PA Canon Kabushiki Kaisha, Tokyo, Japan (non-U.S. corporation)
PI US 5719027 19980217
AI US 1996-605624 19960222 (8)
RLI Division of Ser. No. US 1994-191931, filed on 4 Feb 1994, now abandoned
PRAI JP 1993-19057 19930205
DT Utility
FS Granted
EXNAM Primary Examiner: Green, Lora M.
LREP Fitzpatrick, Cella, Harper & Scinto
CLMN Number of Claims: 7
ECL Exemplary Claim: 1
DRWN 3 Drawing Figure(s); 3 Drawing Page(s)
LN.CNT 915
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A labeled complex formed by combining a labeling agent with a biological substance, where the labeling agent is a trinucleus dye represented by the general formula (I)' or (II)':

ring(Xa)-La-ring(Xb)-Lb-ring(Xc) (I)'

[ring(Xa)-La-ring(Xb)-Lb-ring(Xc)].sup..sym. Y.sup..crclbar.(II)'

where the ring(Xa), ring(Xb), and ring(Xc), which mean rings having Xa, Xb, or Xc respectively, are independently a heterocyclic ring having one to three heteroatoms of oxygen, sulfur, nitrogen, or selenium, the heterocyclic ring being unsubstituted or substituted by any of a substituted or unsubstituted alkyl group, a substituted or unsubstituted aryl group, and a substituted or unsubstituted aralkyl group; La and Lb are independently a methine chain composed of one to six substituted or unsubstituted methine linkage, and one of La and Lb may be omitted to link directly the heterocyclic rings; and Y.sup..crclbar. represents an anion.

A method of analysis, comprises combining any of the labeled complex with a target substance to be detected, and detecting the target substance optically.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L28 ANSWER 16 OF 16 USPATFULL
AN 96:80407 USPATFULL
TI Haptenic probes for detecting capture polynucleotides
IN Adams, Craig W., Corona, CA, United States
PA Beckman Instruments, Inc., Fullerton, CA, United States (U.S. corporation)
PI US 5552541 19960903
AI US 1990-541143 19900620 (7)
DT Utility
FS Granted
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Marschel, Ardin H.
LREP May, William H., Henry, Janis C.
CLMN Number of Claims: 7
ECL Exemplary Claim: 1
DRWN 9 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 1552
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB **Nucleic acid** probes and protein probes are disclosed. The **nucleic acid** probe comprises a probe polynucleotide, a charged hapten label, and a binding moiety. The protein probe comprises a probe protein, a charged hapten label and a binding moiety. The charged hapten label joint to the binding moiety can comprise a negatively charged sulfophenylhydrazine tag compound. Polyclonal antibodies and monoclonal antibodies with specific affinity for the charged hapten labels are disclosed as are hybridomas capable of making the monoclonal antibodies. Methods and kits are disclosed for making the **nucleic acid** probes, making the protein probes, detecting a capture polynucleotide of the **nucleic acid** probe and detecting a capture molecule of the protein probe.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d l28 16 kwic

L28 ANSWER 16 OF 16 USPATFULL
AB **Nucleic acid** probes and protein probes are disclosed. The **nucleic acid** probe comprises a probe polynucleotide, a charged hapten label, and a binding moiety. The

protein probe comprises a probe protein,. . . labels are disclosed as are hybridomas capable of making the monoclonal antibodies. Methods and kits are disclosed for making the **nucleic acid** probes, making the protein probes, detecting a capture polynucleotide of the **nucleic acid** probe and detecting a capture molecule of the protein probe.

SUMM The present invention is directed to novel **nucleic acid** probes and protein probes. The invention is also directed to particular novel polyclonal and monoclonal antibodies useful for detecting the. . .

SUMM **Nucleic acid** probes, also called hybridization probes, allow specific polynucleotide sequences to be detected. Protein probes make possible detection of various compounds,. . .

SUMM **Nucleic acid** probes can be used to detect specific polynucleotide sequences and can assist the diagnosis and treatment of numerous genetic disorders. . .

SUMM **Nucleic acid** probes can also reveal genes coding antigens responsible for graft rejection. Genetic information useful in cancer oncogeny testing and forensic. . .

SUMM . . . I autoradiography. Furthermore, the .sup.32 P isotope is a hazardous isotope. Hence, there is a need for nonradioactive labels for **nucleic acid** and protein probes.

SUMM . . . time, a "stickiness" or aggregation problem is encountered with biotin labels. Stickiness refers to the situation wherein biotinylated antibodies and/or **nucleic acid** probes aggregate due to the change in the surface characteristics of normally charged polynucleotides conjugated to neutral (uncharged) biotin. The. . .

SUMM . . . been sought for incorporation into probes to address these problems. The nonradioactive label can also be useful as an alternate **nucleic acid** and protein probe label. When biotin alternative labels are used in conjunction with biotinylated probes, sandwich assays can be performed. . .

SUMM The term "polynucleotide" is used interchangeably with the term "**nucleic acid**" and includes all oligonucleotides.

SUMM . . . is a 4-hydrazinobenzenesulfonate anion compound covalently attached through its hydrazine terminus to the 4-position of a cytosine base of single-stranded **nucleic acid**. This **nucleic acid** probe can be made under mild conditions and its use allows detection of picogram amounts of capture polynucleotide.

SUMM The present invention satisfies the prior-art need for a **nucleic acid** label and a protein probe label that, when joined to a binding moiety, is soluble, stable, reactive, haptenic, nonradioactive and. . .

DRWD . . . the results of in situ detection of HPV 6 DNA in a human cervical biopsy tissue specimen using a sulfophenyl-labeled **nucleic acid** probe.

DETD . . . that certain compounds can function as superior nonradioactive haptenic labels for labeling polynucleotides. The labeled polynucleotides can be used as **nucleic acid** probes. **Nucleic acid** probes, or hybridization probes as they are also called, can be used to detect specific polynucleotide sequences. Specific polynucleotide sequences. . .

DETD The probe polynucleotide can be DNA or RNA and is preferably a single-stranded **nucleic acid**. The attaching reaction whereby the label is attached to the probe polynucleotide is more difficult with a double-stranded **nucleic acid**.

DETD . . . negatively charged. A negative charge has been found to help reduce the "stickiness" or aggregation problem encountered with neutral or **positively charged labels**. A preferred label is a haptenic, anionic sulfophenyl compound, commercially available and generally stable at room temperature.

DETD . . . can be, for example, an antibody, antigen, hormone, steroid, carbohydrate, enzyme inhibitor, enzyme effector, various enzyme substrate analogues, and a **nucleic acid**.

DETD A hybridization probe was made by attaching sulfophenylhydrazine to a cytosine base-containing **nucleic acid** in an attaching reaction. The sulfophenylhydrazine was used in a labeling mix. The reagents used to prepare the labeling mix. . .

DETD . . . supernatant contains antisulfophenyl antibody conjugated to alkaline phosphatase. This complex can be used to detect the sulfophenyl label of a **nucleic acid** probe or of a protein probe. Improved detection of smaller amounts of sulfophenyl label can be possible because the enzyme. . .

DETD . . . methods that can be used to detect a capture polynucleotide or capture molecule that has reacted with, respectively, a sulfophenyl-labeled **nucleic acid** probe or a sulfophenyl-labeled protein probe. Enzymes, enzyme conjugates, haptens, and nonhaptenic labels different from those set forth but known. . .

DETD **Nucleic acid** probes and protein probes according to the present invention have many advantages including the following:

DETD 4. No purification of the **nucleic acid** is required before the **nucleic acid** is labeled.

=> s positiv? (a) charg? phosphoramidite
L30 2 POSITIV? (A) CHARG? PHOSPHORAMIDITE

=> d l30 bib abs 1-2

L30 ANSWER 1 OF 2 WPIDS (C) 2002 THOMSON DERWENT
AN 2002-674850 [72] WPIDS
CR 1997-393613 [36]
DNC C2002-190055
TI Composition useful for e.g. separation of nucleic acids comprises a positively or neutrally charged phosphoramidite.
DC B04 B05 D16
IN ALLAWI, H T; LYAMICHEV, V; NERI, B P; SKRZPCZYNSKI, Z; TAKOVA, T; WAYLAND, S R
PA (THIR-N) THIRD WAVE TECHNOLOGIES INC
CYC 100
PI WO 2002063030 A2 20020815 (200272)* EN 197p
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW
US 2002128465 A1 20020912 (200272)
ADT WO 2002063030 A2 WO 2002-US3423 20020206; US 2002128465 A1 CIP of US 1996-682853 19960712, CIP of US 1999-333145 19990614, US 2001-777430 20010206
FDT US 2002128465 A1 CIP of US 6001567
PRAI US 2001-777430 20010206; US 1996-682853 19960712; US 1999-333145 19990614
AN 2002-674850 [72] WPIDS
CR 1997-393613 [36]
AB WO 200263030 A UPAB: 20021108
NOVELTY - Composition comprises a positively or neutrally charged phosphoramidite.
DETAILED DESCRIPTION - Composition (c) or (c') comprises a **positively charged phosphoramidite** of formula (I) or a neutrally charged phosphoramidite of formula (II). (I) comprises

nitrogen-containing chemical group selected from primary, secondary or tertiary amine or ammonium group. (II) comprises secondary or tertiary amine or ammonium group.

X, Z = a reactive phosphate group;
Y = a protected hydroxy group;
X' = a protected hydroxy group;
N, N' = an amine group.

INDEPENDENT CLAIMS are included for the following:

(1) a composition (c1) comprising a charge tag (x1) attached to a terminal end of a nucleic acid molecule, the charge tag comprises a phosphate group and a positively charged molecule;

(2) a composition (c2) comprising a nucleic acid molecule that comprises a **positively charged phosphoramidite**
;

(3) a composition (c3) comprising a charge tag attached to the terminal end of a nucleic acid molecule, the charge tag comprises a **positively charged phosphoramidite**;

(4) a composition (c4) comprising a fluorescent dye directly bonded to a phosphate group, which is not directly bonded to an amine group;

(5) a mixture (m) comprising a number of oligonucleotides, each oligonucleotide is attached to a different charge tag with each charge tag comprising a phosphate group and a positively charged group;

(6) a composition (c5) comprising a solid support attached to a charged tag, the charge tag comprises a positively charged group and a reactive group configured to allow the charge tag to covalently attach to the nucleic acid molecule;

(7) separating nucleic acid molecules involving either:

(a) treating (m1) a charge-balanced oligonucleotide containing the charge tag to produce a charge-unbalanced oligonucleotide and separating the charge-unbalanced oligonucleotide from the reaction mixture; or

(b) treating (m2) a number of charge-balanced oligonucleotides, each containing different charge tags, to produce at least 2 charge-unbalanced oligonucleotides, and separating the charge-unbalanced oligonucleotides from the reaction mixture.

USE - The composition is useful for separation of nucleic acid molecules (claimed). The composition is further useful for fractionation of specific nucleic acids by selective charge reversal useful in e.g. INVADER assay cleavage reactions; and in the synthesis of charge-balanced molecules.

ADVANTAGE - In the fractionation of nucleic acid molecules, the method provides an absolute readout of the partition of products from substrates (i.e. provides a 100% separation). Through the use of multiple positively charged adducts, synthetic molecules can be constructed with sufficient modification due to the fact that the normally negatively charged strand is made nearly neutral. It is also possible to distinguish between a enzymatically or thermally degraded DNA fragments due to the absence or presence of 3'phosphate.

Dwg.0/46

L30 ANSWER 2 OF 2 USPATFULL
AN 2002:236261 USPATFULL
TI Charge tags and the separation of nucleic acid molecules
IN Lyamichev, Victor, Madison, WI, UNITED STATES
Skrzpczynski, Zbigniew, Verona, WI, UNITED STATES
Allawi, Hatim T., Madison, WI, UNITED STATES
Wayland, Sarah R., Madison, WI, UNITED STATES
Takova, Tsetska, Madison, WI, UNITED STATES
Neri, Bruce P., Madison, WI, UNITED STATES
PA Third Wave Technologies, Inc. (U.S. corporation)
PI US 2002128465 A1 20020912
AI US 2001-777430 A1 20010206 (9)
RLI Continuation-in-part of Ser. No. US 1999-333145, filed on 14 Jun 1999,

09567863

PENDING Continuation-in-part of Ser. No. US 1996-682853, filed on 12 Jul 1996, GRANTED, Pat. No. US 6001567
DT Utility
FS APPLICATION
LREP MEDLEN & CARROLL, LLP, 101 HOWARD STREET, SUITE 350, SAN FRANCISCO, CA, 94105
CLMN Number of Claims: 86
ECL Exemplary Claim: 1
DRWN 46 Drawing Page(s)
LN.CNT 5163
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The present invention relates to novel phosphoramidites, including positive and neutrally charged compounds. The present invention also provides charge tags for attachment to materials including solid supports and nucleic acids, wherein the charge tags increase or decrease the net charge of the material. The present invention further provides methods for separating and characterizing molecules based on the charge differentials between modified and unmodified materials.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

=> d his

(FILE 'HOME' ENTERED AT 10:12:59 ON 18 DEC 2002)

FILE 'BIOSIS, MEDLINE, CAPLUS, WPIDS, USPATFULL' ENTERED AT 10:13:34 ON 18 DEC 2002

L1 343861 S NUCLEIC ACID
L2 2 S L1 AND POSITIV? (3A) CHARGE TAG (3A) NUCLEIC ACID?
L3 21 S L1 AND POSITIV? (4A) CHARG? (3A) TAG?
L4 19 S L3 NOT L2
L5 19 DUP REM L4 (0 DUPLICATES REMOVED)
L6 109 S L1 AND POSITIV? (4A) LABEL
L7 108 S L6 NOT L5
L8 92 S L7 AND PHOSPHAT?
L9 92 DUP REM L8 (0 DUPLICATES REMOVED)
L10 22 S L9 AND POSITIV? (4A) CHARG?
L11 1 S POSITIV? (3A) CHARG? (3A) LABEL? (4A) TERMINAL (4A) (NUCLEIC
L12 1 S L11 AND POSITIV?
L13 110 S MASS TAG
L14 50 S L13 AND OLIGONUCLEOTIDE?
L15 43 S L14 AND LABEL?
L16 21 S L15 AND TERMINAL
L17 21 DUP REM L16 (0 DUPLICATES REMOVED)
L18 1 S POSITIV? CHARG? LABEL? OLIGONUCLEOTIDE?
L19 1 S POSITIV? (4A) CHARG? LABEL? (3A) OLIGONUCLEOTIDE?
L20 117 S POSITIV? (5A) (LABEL? OR TAG?) (4A) OLIGONUCLEOTIDE?
L21 31 S L20 AND AMINE
L22 23 S L21 AND AMMONIUM
L23 2 S L22 AND PHOSPHORAMIDITE
L24 21 S L22 NOT L23
L25 25 S POSITIV? (3A) CHARG? (3A) PHOSPHORAMIDITE?
L26 25 DUP REM L25 (0 DUPLICATES REMOVED)
L27 21 S POSITIV? CHARG? LABEL?
L28 16 S L27 AND NUCLEIC ACID
L29 1 S L28 AND POSITIV? (2A) PHOSPHORAMIDITE
L30 2 S POSITIV? (A) CHARG? PHOSPHORAMIDITE

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=>
=> s l32 and charg?
L33          9 L32 AND CHARG?

=> d l33 bib abs 1-9

L33  ANSWER 1 OF 9  WPIDS (C) 2002 THOMSON DERWENT
AN   2002-706900 [76]   WPIDS
DNC  C2002-200480
TI   Preparation of oligonucleotides used as diagnostic agents, research
     reagents and therapeutics comprises reacting nucleoside
     phosphoramidite with a support bound oligomer in presence of
     neutralizing agent.
DC   B03 B04
IN   GUZAEV, A P; MANOHARAN, M
PA   (GUZA-I) GUZAEV A P; (MANO-I) MANOHARAN M; (ISIS-N) ISIS PHARM INC
CYC  98
PI   WO 2002062811 A2 20020815 (200276)* EN   92p
        RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ
            NL OA PT SD SE SL SZ TR TZ UG ZM ZW
         W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK
            DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR
            KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PL PT RO
            RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZM ZW
     US 2002147331 A1 20021010 (200276)
ADT  WO 2002062811 A2 WO 2002-US2336 20020128; US 2002147331 A1 US 2001-775967
     20010202
PRAI US 2001-775967   20010202
AN   2002-706900 [76]   WPIDS
AB   WO 200262811 A UPAB: 20021125
     NOVELTY - Preparation of oligonucleotides comprises reacting a nucleoside
     phosphoramidite with a support bound oligomer having at least one
     unprotected internucleoside linkage in the presence of a neutralizing
     agent (A) comprising e.g. aliphatic amine, aliphatic
     heterocyclic amine or aromatic amine.
          DETAILED DESCRIPTION - Preparation of oligonucleotides comprises
     reacting a nucleoside phosphoramidite with a support bound oligomer having
     at least one unprotected internucleoside linkage comprising a phosphate
     linkage, phosphorothioate linkage or phosphorodithioate linkage, in the
     presence of a neutralizing agent comprising an aliphatic amine,
     aliphatic heterocyclic amine, aromatic amine, aromatic
     heterocyclic amine, guanidine or a salt of formula D+E-.
          D+ = quaternary tetraalkylammonium cation or a protonated aliphatic
     amine, aliphatic heterocyclic amine, aromatic
     amine, aromatic heterocyclic amine or guanidine, and
          E- = tetrazolide anion, 4,5-dicyanoimidazolide anion, optionally
     substituted alkylsulfonate anion, optionally substituted arylsulfonate
     anion, tetrafluoroborate anion, hexafluorophosphate anion or
     trihaloacetate anion.
          INDEPENDENT CLAIMS are included for the following:
          (1) forming an internucleoside linkage which comprises reacting a
     phosphoramidite of formula (I) with a compound of formula (II) in the
     presence of (A);
          (2) a method which comprises deprotecting the 5'-hydroxyl group of a
     solid support having a 5'-O-protected phosphorus-linked oligomer having at
     least one phosphoryl internucleoside linkage that does not have a
     phosphoryl protecting group, washing with a solution containing (A),
     reacting the free hydroxyl with a 5'-protected nucleoside phosphoramidite
     to form a phosphite triester linkage and oxidizing or sulfurizing the
     covalent linkage to form a phosphodiester, phosphorothioate,
     phosphorodithioate or H-phosphonate linkage, and
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(3) a composition comprising a 5'-protected nucleoside phosphoramidite and D+E-.
L1 = an internucleoside linkage;
n1 = 0-100;
R1 = OH protecting group;
R2 = 2'-substituent group;
R4, R5 = 1-10C alkyl or
NR4R5 = heterocyclyl;
B = a nucleobase;
Q, Z, X = O or S;
Pg = phosphoryl protecting group;
R3 = a linker connected to a solid support;
n = 1-100;
L = O-P(=X)(-Z-Y)-O, and
Y = phosphoryl protecting group or a negative **charge**, provided that at least one is a negative **charge**.
ACTIVITY - None given in the source material.
MECHANISM OF ACTION - Transcription factor inhibitor; Gene therapy.
USE - Useful as diagnostic reagents, research reagents and therapeutics for modulating the action of transcriptase factors.
ADVANTAGE - The method avoids the need for phosphoryl protecting groups.
Dwg.0/22

L33 ANSWER 2 OF 9 WPIDS (C) 2002 THOMSON DERWENT
AN 2002-674850 [72] WPIDS
CR 1997-393613 [36]
DNC C2002-190055
TI Composition useful for e.g. separation of nucleic acids comprises a positively or neutrally **charged phosphoramidite**.
DC B04 B05 D16
IN ALLAWI, H T; LYAMICHEV, V; NERI, B P; SKRZPCZYNSKI, Z; TAKOVA, T; WAYLAND, S R
PA (THIR-N) THIRD WAVE TECHNOLOGIES INC
CYC 100
PI WO 2002063030 A2 20020815 (200272)* EN 197p
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW
US 2002128465 A1 20020912 (200272)
ADT WO 2002063030 A2 WO 2002-US3423 20020206; US 2002128465 A1 CIP of US 1996-682853 19960712, CIP of US 1999-333145 19990614, US 2001-777430 20010206
FDT US 2002128465 A1 CIP of US 6001567
PRAI US 2001-777430 20010206; US 1996-682853 19960712; US 1999-333145 19990614
AN 2002-674850 [72] WPIDS
CR 1997-393613 [36]
AB WO 200263030 A UPAB: 20021108
NOVELTY - Composition comprises a positively or neutrally **charged** phosphoramidite.
DETAILED DESCRIPTION - Composition (c) or (c') comprises a positively **charged** phosphoramidite of formula (I) or a neutrally **charged** phosphoramidite of formula (II). (I) comprises nitrogen-containing chemical group selected from primary, secondary or tertiary **amine** or ammonium group. (II) comprises secondary or tertiary **amine** or ammonium group.
X, Z = a reactive phosphate group;

Y = a protected hydroxy group;
X' = a protected hydroxy group;
N, N' = an **amine** group.
INDEPENDENT CLAIMS are included for the following:
(1) a composition (c1) comprising a **charge** tag (x1) attached to a terminal end of a nucleic acid molecule, the **charge** tag comprises a phosphate group and a positively **charged** molecule;
(2) a composition (c2) comprising a nucleic acid molecule that comprises a positively **charged** phosphoramidite;
(3) a composition (c3) comprising a **charge** tag attached to the terminal end of a nucleic acid molecule, the **charge** tag comprises a positively **charged** phosphoramidite;
(4) a composition (c4) comprising a fluorescent dye directly bonded to a phosphate group, which is not directly bonded to an **amine** group;
(5) a mixture (m) comprising a number of oligonucleotides, each oligonucleotide is attached to a different **charge** tag with each **charge** tag comprising a phosphate group and a positively **charged** group;
(6) a composition (c5) comprising a solid support attached to a **charged** tag, the **charge** tag comprises a positively **charged** group and a reactive group configured to allow the **charge** tag to covalently attach to the nucleic acid molecule;
(7) separating nucleic acid molecules involving either:
(a) treating (m1) a **charge**-balanced oligonucleotide containing the **charge** tag to produce a **charge**-unbalanced oligonucleotide and separating the **charge**-unbalanced oligonucleotide from the reaction mixture; or
(b) treating (m2) a number of **charge**-balanced oligonucleotides, each containing different **charge** tags, to produce at least 2 **charge**-unbalanced oligonucleotides, and separating the **charge**-unbalanced oligonucleotides from the reaction mixture.
USE - The composition is useful for separation of nucleic acid molecules (claimed). The composition is further useful for fractionation of specific nucleic acids by selective **charge** reversal useful in e.g. INVADER assay cleavage reactions; and in the synthesis of **charge**-balanced molecules.
ADVANTAGE - In the fractionation of nucleic acid molecules, the method provides an absolute readout of the partition of products from substrates (i.e. provides a 100% separation). Through the use of multiple positively **charged** adducts, synthetic molecules can be constructed with sufficient modification due to the fact that the normally negatively **charged** strand is made nearly neutral. It is also possible to distinguish between a enzymatically or thermally degraded DNA fragments due to the absence or presence of 3'phosphate.
Dwg.0/46

L33 ANSWER 3 OF 9 USPATFULL
AN 1999:13039 USPATFULL
TI **Phosphoramidite** derivatives, their preparation and the use thereof in the incorporation of reporter groups on synthetic oligonucleotides
IN Misiura, Konrad, Lodz, Poland
Gait, Michael J., Cambridge, Great Britain
PA Amersham International plc, Buckinghamshire, England (non-U.S. corporation)
PI US 5864032 19990126
AI US 1995-406700 19950320 (8)
RLI Division of Ser. No. US 1992-946477, filed on 3 Nov 1992, now patented, Pat. No. US 5567811

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PRAI GB 1990-9980 19900503
DT Utility
FS Granted
EXNAM Primary Examiner: Elliott, George G.; Assistant Examiner: Houtteman, Scott W.
LREP Wenderoth, Lind & Ponack
CLMN Number of Claims: 6
ECL Exemplary Claim: 1
DRWN 11 Drawing Figure(s); 9 Drawing Page(s)
LN.CNT 1119
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Phosphoramidite derivatives of formula (V), ##STR1## wherein X is biotin and Y is a protecting group. There may be a linker arm, of variable length, between X and the rest of the molecule. Examples of the protecting group Y include 4,4'-dimethoxytrityl, trifluoroacetyl and fluorenylmethoxycarbonyl (Fmoc). The phosphoramidite derivatives are useful in single or multiple labelling of synthetic oligonucleotides. Process for the preparation of these phosphoramidite derivatives are also disclosed.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L33 ANSWER 4 OF 9 USPATFULL
AN 1998:144261 USPATFULL
TI **Phosphoramidite** derivatives of macrocycles
IN Magda, Darren, Cupertino, CA, United States
Sessler, Jonathan L., Austin, TX, United States
Crofts, Shaun P., Campbell, CA, United States
PA Board of Regents, The University of Texas, Austin, TX, United States (U.S. corporation)
Pharmacyclics, Inc., Sunnyvale, CA, United States (U.S. corporation)
PI US 5837866 19981117
AI US 1997-862778 19970523 (8)
RLI Continuation-in-part of Ser. No. US 1996-614638, filed on 13 Mar 1996, now patented, Pat. No. US 5633354 which is a continuation of Ser. No. US 1995-487722, filed on 7 Jun 1995, now patented, Pat. No. US 5565552 which is a continuation-in-part of Ser. No. US 1994-310501, filed on 21 Sep 1994, now patented, Pat. No. US 5567587
DT Utility
FS Granted
EXNAM Primary Examiner: Raymond, Richard L.
LREP Larson, Jacqueline S.
CLMN Number of Claims: 12
ECL Exemplary Claim: 1
DRWN 8 Drawing Figure(s); 8 Drawing Page(s)
LN.CNT 1195
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention is directed to phosphoramidite derivatives of macrocycles, such as porphyrins and expanded porphyrins, including sapphyrins and texaphyrins. The phosphoramidite derivatives are useful as intermediates in the preparation of macrocycle-oligonucleotide conjugates.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L33 ANSWER 5 OF 9 USPATFULL
AN 97:45114 USPATFULL
TI **Phosphoramidite** derivatives of texaphyrins
IN Magda, Darren, Cupertino, CA, United States
Sessler, Jonathan L., Austin, TX, United States
Iverson, Brent L., Austin, TX, United States
Sansom, Petra I., Austin, TX, United States
Crofts, Shaun P., Campbell, CA, United States

09567863

PA Pharmacyclics, Inc., Sunnyvale, CA, United States (U.S. corporation)
Board of Regents, The University of Texas, Austin, TX, United States (U.S. corporation)
PI US 5633354 19970527
AI US 1996-614638 19960313 (8)
RLI Continuation of Ser. No. US 1995-487722, filed on 7 Jun 1995, now patented, Pat. No. US 5565552 which is a continuation-in-part of Ser. No. US 1994-310501, filed on 21 Sep 1994, now patented, Pat. No. US 5567687
DT Utility
FS Granted
EXNAM Primary Examiner: Raymond, Richard L.
LREP Larson, Jacqueline S.
CLMN Number of Claims: 18
ECL Exemplary Claim: 1
DRWN 7 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 996
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB The invention is directed to a method of incorporating expanded porphyrins, and particularly of incorporating a sapphyrin or a texaphyrin, before, during, or after chemical synthesis of an oligomer to form an expanded porphyrin-oligonucleotide conjugate, and particularly a sapphyrin- or texaphyrin-oligonucleotide conjugate. This method includes reacting derivatized nucleotides and a sapphyrin or a texaphyrin in a desired order in an automated or manual DNA synthesizer having a solid support to form a sapphyrin- or a texaphyrin-oligonucleotide conjugate.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L33 ANSWER 6 OF 9 USPATFULL
AN 96:97145 USPATFULL
TI **Phosphoramidite** derivatives, their preparation and the use thereof in the incorporation of reporter groups on synthetic oligonucleotides
IN Misiura, Konrad, Lodz, Poland
Gait, Michael, Cambridge, Great Britain
PA Amersham International plc, England (non-U.S. corporation)
PI US 5567811 19961022
WO 9117169 19911114
AI US 1992-946477 19921103 (7)
WO 1991-GB713 19910503
19921103 PCT 371 date
19921103 PCT 102(e) date
PRAI GB 1990-9980 19900503
DT Utility
FS Granted
EXNAM Primary Examiner: Jones, W. Gary; Assistant Examiner: Houtteman, Scott
LREP Wenderoth, Lind & Ponack
CLMN Number of Claims: 6
ECL Exemplary Claim: 1
DRWN 11 Drawing Figure(s); 9 Drawing Page(s)
LN.CNT 1128
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Phosphoramidite derivatives of formula (V), ##STR1## wherein X is biotin and Y is a protecting group. There may be a linker arm, of variable length, between X and the rest of the molecule. Examples of the protecting group Y include 4,4'-dimethoxytrityl, trifluoroacetyl and fluorenylmethoxycarbonyl (Fmoc). The phosphoramidite derivatives are useful in single or multiple labelling of synthetic oligonucleotides. Process for the preparation of these phosphoramidite derivatives are also disclosed.

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CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L33 ANSWER 7 OF 9 USPATFULL
AN 91:50608 USPATFULL
TI **Phosphoramidite** compounds and process for production thereof
IN Nojiri, Ryuji, Aichi, Japan
Hayakawa, Yoshihiro, Ichinomiya, Japan
Uchiyama, Mamoru, Kawasaki, Japan
Kato, Hisatoyo, Ohbu, Japan
Chino, Yasuyoshi, Tokyo, Japan
Tahara, Shinichiro, Yokohama, Japan
PA Nippon Zeon Co., Ltd., Tokyo, Japan (non-U.S. corporation)
PI US 5026838 19910625
AI US 1988-229773 19880804 (7)
RLI Continuation of Ser. No. US 1986-909728, filed on 22 Sep 1986, now abandoned
PRAI JP 1985-211240 19850925
JP 1985-223138 19851007
DT Utility
FS Granted
EXNAM Primary Examiner: Brown, Johnnie R.; Assistant Examiner: Crane, L. Eric
LREP Sherman & Shalloway
CLMN Number of Claims: 14
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 855
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Phosphoramidite compounds of the general formula ##STR1## wherein each of R.sub.1 and R.sub.2 represents a hydroxyl group having a protective group, or the group --OR.sub.4, R.sub.3 represents a hydrogen atom, a hydroxyl group having a protective group, or the group --OR.sub.4, R.sub.4 represents the group ##STR2## X represents a secondary amino group, R.sub.5 represents an allylic residue or a protective group capable of being split off by beta-cleavage, and B.sup.AOC represents a nucleoside base residue in which the amino or imino group is protected with an allyloxycarbonyl-type residue, with the proviso that only one of R.sub.1, R.sub.2 and R.sub.3 represents the group--OR.sub.4. The compounds can be produced by reacting a nucleoside represented by the general formula ##STR3## wherein each of R.sub.1 ' and R.sub.2 ' represents a hydroxyl group which may have a protective group, R.sub.3 ' represents a hydrogen atom, or a hydroxyl group which may have a protective group, and B.sup.AOC is as defined, with the proviso that only one of R.sub.1 ', R.sub.2 'and R.sub.3 ' is a hydroxyl group,

with a phosphoramide compound represented by the general formula ##STR4## wherein X and R.sub.5 are as defined, and Y represents a secondary amino group or a halogen atom.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L33 ANSWER 8 OF 9 USPATFULL
AN 87:38081 USPATFULL
TI **Phosphoramidite** nucleoside compounds
IN Caruthers, Marvin H., Boulder, CO, United States
Beaucage, Serge L., Mountain View, CA, United States
PA University Patents, Inc., Westport, CT, United States (U.S. corporation)
PI US 4668777 19870526
AI US 1984-637927 19840806 (6)
DCD 20001115
RLI Continuation of Ser. No. US 1982-358589, filed on 16 Mar 1982, now abandoned which is a continuation-in-part of Ser. No. US 1981-248450,

filed on 27 Mar 1981, now patented, Pat. No. US 4415732
DT Utility
FS Granted
EXNAM Primary Examiner: Brown, Johnnie R.; Assistant Examiner: Peselev, Elli
LREP Yahwak, George M.
CLMN Number of Claims: 25
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 1059
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A new class of nucleoside phosphoramidites which are relatively stable to permit isolation thereof and storage at room temperature. The phosphoramidites are derivatives of saturated secondary amines.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L33 ANSWER 9 OF 9 USPATFULL
AN 83:53604 USPATFULL
TI **Phosphoramidite** compounds and processes
IN Caruthers, Marvin H., Boulder, CO, United States
Beaucage, Serge L., Boulder, CO, United States
PA University Patents, Inc., Norwalk, CT, United States (U.S. corporation)
PI US 4415732 19831115
AI US 1981-248450 19810327 (6)
DT Utility
FS Granted
EXNAM Primary Examiner: Love, Ethel G.
LREP Scully, Scott, Murphy & Presser
CLMN Number of Claims: 20
ECL Exemplary Claim: 1
DRWN No Drawings
LN.CNT 553
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A new class of nucleoside phosphoramidites which are relatively stable to permit isolation thereof and storage at room temperature. The phosphoramidites are derivatives of saturated secondary amines.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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L33 ANSWER 9 OF 9 USPATFULL
TI **Phosphoramidite** compounds and processes
SUMM . . . heteroatoms such as N, S or O. These compounds of structure II and IIa wherein X is such a heterocyclic **amine**, i.e., one in which the amino nitrogen is a ring heteroatom, are characterized by an extremely high reactivity, and consequently. . .
SUMM . . . compounds of the present invention can be prepared according to art-recognized procedures such as by reaction of the selected secondary **amine** with the corresponding nucleoside phosphomonochloridite. This reaction is accomplished by dissolving the said nucleoside in an organic solvent, such as tetrahydrofuran or acetonitrile, and adding the selected secondary **amine**. After removing unwanted hydrochloride salt, the organic solvent solution of the phosphoramidite may be used as such for polynucleotide synthesis. . .
SUMM . . . chloro-(2.degree. amino)alkyoxyphosphine is effected in an organic solvent solution of the selected nucleoside, preferably in the presence of a tertiary **amine** to take up the hydrogen chloride formed in the condensation reaction. The reaction proceeds smoothly at room temperature in a. . . ethyl acetate, and the like. The solution of product is separated from the precipitated hydrochloride salt of the

added tertiary **amine** and can be used as such in forming polynucleotide or alternatively can be separated from the solvent and purified as. . .

SUMM . . . acidic compounds to be employed for the purpose of the said activation are preferably mildly acidic and include, for example, **amine** hydrohalide salts and nitrogen heterocyclic compounds such as tetrazoles, imidazoles, nitroimidazoles, benzimidazoles and similar nitrogen heterocyclic proton donors. The **amine** hydrohalide salts to be used for the protonation activation are preferably tertiary **amine** salts, and, preferably, the hydrochloride salts, although hydrobromide, hydroiodide or hydrofluoride salts can also be used. The aforesaid tertiary amines. . .

SUMM When the nucleoside is guanosine, i.e. where B is guanine, the use of **amine** hydrochlorides is not very effective for the purpose of activation, i.e. by protonation. With those compounds in which B is. . .

DETD . . . chloro-N, N-dimethylaminomethoxyphosphine [CH.sub.3 O P(Cl) N(CH.sub.3).sub.2] which is used a monofunctional phosphitylating agent. A 250 ml addition funnel was **charged** with 100 ml of precooled anhydrous ether (-78.degree. C.) and pre-cooled (-78.degree. C.) anhydrous dimethylamine (45.9 g, 1.02 mol). The. . . caps tightened with copper wire. The suspension was mechanically stirred for 2 h at room temperature, then filtered and the **amine** hydrochloride salt washed with 500 ml anhydrous ether. The combined filtrate and washings were distilled at atmospheric pressure and the. . .

DETD . . . were employed in condensation with 3'-O-blocked nucleosides to form internucleotide bonds. The phosphoramidites were activated by weak acids such as **amine** hydrochloride salts or tetrazoles.

DETD A 50 ml dropping funnel was **charged** with 31.59 g of N, N-Dimethylaminotrimethylsilane (42.1 ml, 0.27 mol) which wad added dropwise over 1 h under nitrogen atmosphere. . .

DETD . . . tetrazolide. The gum resulting from the final re-evaporation is dissolved in THF (2 ml). A solution of the selected secondary **amine** 0.9 mmole) in THF (2 ml) is then added dropwise with stirring at -78.degree. C. to the nucleoside phosphomonochloridite. After. . .

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(FILE 'HOME' ENTERED AT 10:12:59 ON 18 DEC 2002)

FILE 'BIOSIS, MEDLINE, CAPLUS, WPIDS, USPATFULL' ENTERED AT 10:13:34 ON 18 DEC 2002

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L1        343861 S NUCLEIC ACID
L2             2 S L1 AND POSITIV? (3A) CHARGE TAG (3A) NUCLEIC ACID?
L3            21 S L1 AND POSITIV? (4A) CHARG? (3A) TAG?
L4            19 S L3 NOT L2
L5            19 DUP REM L4 (0 DUPLICATES REMOVED)
L6           109 S L1 AND POSITIV? (4A) LABEL
L7           108 S L6 NOT L5
L8            92 S L7 AND PHOSPHAT?
L9            92 DUP REM L8 (0 DUPLICATES REMOVED)
L10           22 S L9 AND POSITIV? (4A) CHARG?
L11            1 S POSITIV? (3A) CHARG? (3A) LABEL? (4A) TERMINAL (4A) (NUCLEIC
L12            1 S L11 AND POSITIV?
L13          110 S MASS TAG
L14           50 S L13 AND OLIGONUCLEOTIDE?
L15           43 S L14 AND LABEL?
L16           21 S L15 AND TERMINAL
L17           21 DUP REM L16 (0 DUPLICATES REMOVED)
L18            1 S POSITIV? CHARG? LABEL? OLIGONUCLEOTIDE?
L19            1 S POSITIV? (4A) CHARG? LABEL? (3A) OLIGONUCLEOTIDE?
L20          117 S POSITIV? (5A) (LABEL? OR TAG?) (4A) OLIGONUCLEOTIDE?
L21           31 S L20 AND AMINE
L22           23 S L21 AND AMMONIUM
L23            2 S L22 AND PHOSPHORAMIDITE
L24           21 S L22 NOT L23
L25           25 S POSITIV? (3A) CHARG? (3A) PHOSPHORAMIDITE?
L26           25 DUP REM L25 (0 DUPLICATES REMOVED)
L27           21 S POSITIV? CHARG? LABEL?
L28           16 S L27 AND NUCLEIC ACID
L29            1 S L28 AND POSITIV? (2A) PHOSPHORAMIDITE
L30            2 S POSITIV? (A) CHARG? PHOSPHORAMIDITE
L31          596 S PHOSPHORAMIDITE/TI
L32           43 S L31 AND AMINE
L33            9 S L32 AND CHARG?
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